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Sequence 69133
Sequence 6133 Application US/09513999C
Sequence 69133 Application US/09513999C
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
FILE REFREENCE: 59.042.REG
CURRENT APPLICATION NUMBER: US/09/513,999C
CURRENT APLICATION NUMBER: US 60/122,487
PRIOR FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SEQ ID NO 6913
LENGTH: 68
                                                                      Sequence 516, 15 Sequence 516, 16 Sequence 516, 16 Sequence 516, 17 Sequence 516, 18 Sequen
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PPQR--NSFFIIYLFUNRDEVSPCCPGWCQSPGLKQSICPGSPKCWDYCRKPP
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TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57036
LENGTH: 836
PCT-USO2-32727-17586
US-10-131-8134-516
US-10-131-8124-516
US-10-131-824A-516
US-10-131-824A-516
US-10-131-824A-516
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US-10-127-813A-516
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US-10-131-833A-516
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Pred. No. 0.098;
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Pred. No. 23;
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ORGANISM: Homo sapiens
US-09-724-676-57036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: Homo sapiens
US-09-513-999C-6913
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Best Local Similarity
Matches 16; Conserv
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Best Local Similarity
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US-09-724-676-57036
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                                                                                                                                                                                           (without alignments)
155.522 Million cell updates/sec
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1: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

2: /cgn2_6/ptodata/2/paa/USO6_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/USO3_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/USO8_NEW_COMB.pep:*

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Compugen Ltd.
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US-09-724-676-57036

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US-09-724-676-53566
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US-09-724-676-53564
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Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Pred. No. 23;
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US-09-724-676-57041
US-09-724-676-57041
Sequence 57041, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: VARIANTS of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 57041
                                                                                                                                                                                                                                                                                                APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEG ID NO $57040
LENGTH: 836
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APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                               Sequence 57040, Application US/09724676 GENERAL INFORMATION:
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32.4%;
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Best Local Similarity 32.4%;
Matches 11; Conservative 4
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1larity 32.4%;
Conservative
                                                        Query Match 19.8'
Best Local Similarity 32.4'
Matches 11; Conservative
   ; ORGANISM: Homo sapiens
US-09-724-676-57039
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Best Local Similarity
Matches 11; Conserv
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US-09-724-676-57040
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TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICANTON NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SEQ ID NO 57037
LENGTH: 836
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GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILIG DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
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TITLE OF INVENTION: Variants of alternative splicing
FILE REPERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
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Pred. No. 23;
4; Mismatches 1:
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23;
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 Mismatches
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                                  3 RONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWA 36
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Pred. No.
                                                                                                                                                                Sequence 57037, Application US/09724676 GENERAL INFORMATION:
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32.4%;
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Best'Local Similarity 32.4%;
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Matches 11; Conservative
Conservative
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; ORGANISM: Homo sapiens
US-09-724-676-57038
                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: Homo sapiens US-09-724-676-57037
                                                                                                                             RESULT 3
US-09-724-676-57037
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LENGTH: 836
11;
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GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENT: Compagen LFD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compagen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEQ ID NO 57077
LENGTH: 836
            TITLE OF INVENTION: Variants of alternative splicing FILE REFERENCE: 129181.4 Compugen CURRENT APPLICATION WOMBER: US/09/724,676 CURRENT FILING DATE: 2000-11-28 NUMBER OF SEQ ID NOS: 97222 SOFTWARE: Patentin version 3.2 SEQ ID NO 57074 LENGTH: 836
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TITLE OF INVENTION: Variants of alternative splicing
FILLE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEGO ID NO 57075
LENGTH: 836
                                                                                                                                                                                                                                                                                                         19;
                                                                                                                                                                                                                                                            Score 57; DB 5;
Pred. No. 23;
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Pred. No. 23;
4; Mismatches 1
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                                                                                                                                                                                                                                                                                                       4; Mismatches
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 12
US-09-724-676-57075
; Sequence 57075, Application US/09724676
; GENERAL INFORMATION:
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ilarity 32.4%;
Conservative
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Best Local Similarity 32.4%;
Matches 11; Conservative
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Best Local Similarity 32.4%;
Matches 11; Conservative
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US-09-724-676-57075
                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-09-724-676-57074
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APPLICANT: Compugen LTD
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Best Local Similarity
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US-09-724-676-57077
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US-09-724-676-57077
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Pred. No. 23;
4; Mismatches 19; Indels
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23;
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GENERAL INFORMATION:
APPLICANT: Compugen LTD:
TTYLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
GURRENT APPLICATION NUMBER: US/09/724,676
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57073
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: Patentin version 3.2
SEOFTWARE: Patentin version 3.2
LENGTH: 836
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US-09-724-676-57072
; Sequence 57072, Application US/09724676
; GENERAL INFORMATION:
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                   SOFTWARE: PatentIn version 3.2
SEQ ID NO 57071
LENGTH: 836
                                                                                                                                                             Query Match 19.8%;
Best Local Similarity 32.4%;
Matches 11; Conservative
NUMBER OF SEQ ID NOS: 97222
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US-09-724-676-57073
                                                                                               ; ORGANISM: Homo sapiens
US-09-724-676-57071
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US-09-724-676-57074
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US-09-724-676-57073
                                                                              TYPE: PRT
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Best Local Similarity 32.4%; Pred. No. 23;
Matches 11; Conservative 4; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 19.8%; Score 57; DB 5; Length 836; Best Local Similarity 32.4%; Pred. No. 23; Matches 11; Conservative 4; Mismatches 19; Indels
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US-09-724-676-57110

Sequence 5710, Application US/09724676

GENERAL INFORATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing
FILE REFERENCE: 129181.4 Compugen
CURRENT APPLICATION UNMER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOTTWARE: PATEANTIN Version 3.2
SEQ ID NO 57110
LENGTH: 836
TYPE: PRT
TYPE: PRT
TYPE: PRT
USGANISM: HOMO Sapiens
US-09-724-676-57110
RESULT 14
US-09-724-676-57108
Sequence 57108, Application US/09724676
GENERAL INFORMATION:
APPLICANT: Compugen LTD
TITLE OF INVENTION: Variants of alternative splicing; FIGE REFERENCE: 1291814 Compugen
CURRENT APPLICATION NUMBER: US/09/724,676
CURRENT FILING DATE: 2000-11-28
NUMBER OF SEQ ID NOS: 97222
SOFTWARE: PatentIn version 3.2
SEQ ID NO 57108
LENGTH: 836
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CAGANISM: Homo sapiens
US-09-724-676-57108
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Search completed: November 22, 2002, 14:30:05 Job time : 12 secs

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288
1 KQRQNKPPSKPNNDFHFEVF.......NNPTCWALCKRIPNKKPGKK
GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                              OM protein - protein search, using sw model
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Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description	Sequence 1, Appli	Sequence 32, Appl	Sequence 36, Appl	Sequence 40, Appl	Sequence 42, Appl	Sequence 43, Appl
		ID	US-09-202-035-1	US-09-202-035-32	US-09-202-035-36	US-09-202-035-40	US-09-202-035-42	US-09-202-035-43
		DB	16	16	16	16	16	16
		Match Length DB	49	49	49	49	49	49
dР	Query	Match	100.0	100.0	100.0	100.0	100.0	100.0
		Score		288	288	288	288	288
	Result	No.		7	m	4	Ŋ	9

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298 27 US=60-208-701-2	49 16 US-09-202-03	16 US-09-202-035-	16 US-09-202-035-	16 US-09-202-035-	16 US-09-202-035-	16_US-09-202-03	20 US-09-647-309A-4	20 US-09-647-30	01 18 US-09-462-918C-4	US-09-647-3	01 23 US-09-936-677-	01 24 US-10-088-72	32 12 US-08-896-44	32 16 US-09-272-262-	32 18 US-09-462-816	98 7 US-08-344-639-8	98 7 US-08-344-639A-	98 7 US-08-344-639C-	98 7 US-08-344-639D	98 8 US-08-467-9	98 8 US-08-467-963-	98 8 US-08-467-963B	98 8 US-08-467-969-	98 12 US-08-834-204-	98 12 US-08-838-	98 12 US-08-838-189A-	98 12 US-08-838-189B-	98 12 US-08-838-189C-	98 12 US-08-838-189D	98 12 US-08-852-344-8	98 12 US-08-852-34	98 12 US-08-852-344B-	98 12 US-08-852-34	98 12 US-08-896-442-	98 16 US-09-272-262	98 18 US-09-462-816-	98 18 US-09-479-240	22 2
88 1	285 99.0	85	85 99.	85 99.	85	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.	85 99.
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RESULT 1

US-09-202-035-1

US-09-202-035-1

US-09-202-035-1

GENERAL INFORMATION:
APPLICART: Joffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: VIRAL PEPSIZORY Syncytial Virus
FILE REFERENCE: 41585200100

CURRENT PILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: US/09/202,035

CURRENT FILING DATE: 1997-06-04

EARLIER FILING DATE: 1996-06-05

BARLIER FILING DATE: 1996-06-05

NUMBER OF SED ID NOS: 44

SOFTWARE: PRT

ORGANISM: respiratory syncytial virus

ONGANISM: respiratory syncytial virus

ONGANISM: Respiratory Syncytial virus

GOGANISM: Respiratory Syncytial Virus

Heart Match
Best Local Similarity 100.0%; Score 288; DB 16; Length 49;
Best Local Similarity 100.0%; Mismatches 0; Indels 0; Gaps 0;
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ORGANISM: respiratory syncytial virus
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Sequence 40, Application US/09202035 GENERAL INFORMATION:
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Best Local Similarity 100.0%; P
Matches 49; Conservative 0;
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; OTHER INFORMATION: amidation
US-09-202-035-42
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SEQ ID NO 40
LENGTH: 49
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OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                            APPLICANT: Jeffrey John Gorman
TIȚLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TIȚLE OF INVENTION: Respiratory Syncytial Virus
TIŢLE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 415852000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: PCT/AU97/00351
EARLIER PILING DATE: 1997-06-04
EARLIER PILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARRE: Patentin Ver. 2.1
SEQ ID NO 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Jeffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 415852000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER PILING DATE: 1999-12-17
EARLIER FILING DATE: 1990-06-05
EARLIER FILING DATE: 1990-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PATENTIN Ver. 2.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 288; DB 16; Length 49; ilarity 100.0%; Pred. No. 1e-25; Conservative 0; Mismatches 0; Indels
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; ORGANISM: respiratory syncytial virus
US-09-202-035-32
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                                                                    Sequence 32, Application US/09202035 GENERAL INFORMATION:
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OTHER INFORMATION: acetylation
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; OTHER INFORMATION: amidation
US-09-202-035-36
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Matches 49; Conser
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NAME/KEY: SITE
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US-09-202-035-36
                                              us-09+202-035-32
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RESULT: 4 i i

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APPLICANT. Jeffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REPERENCE: 41585200100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1997-06-04
EARLIER PELICATION NUMBER: PCT/AU97/00351
EARLIER FILING DATE: 1997-06-04
EARLIER FILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 44
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OTHER INFORMATION: benzoyl benzylamide derivatisation
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Pred. No. 1e-25;
; Mismatches 0;
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RESULT 9

US-09-202-035-3

IS-GQUENCE 3, Application US/09202035

GENERAL INFORMATION:

APPLICANT: Jeffrey John Gorman

TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of

TITLE OF INVENTION: Viral Peptides With Structural Homology to Protein G of

TITLE OF INVENTION: Wiral Peptides With Structural Homology to Protein G of

TITLE OF INVENTION: VIVAL RESPIRATE ALS BS 2000100

CURRENT APPLICATION NUMBER: PCT/AU97/00351

EARLIER FILING DATE: 1998-12-17

EARLIER FILING DATE: 1996-06-05

SERLIER FILING DATE: 1996-06-05

NUMBER OF SEQ ID NOS: 44

SEPTWARE: PatentIn Ver: 2.1
                                                   APPLICATE: Jeffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
TITLE OF INVENTION: Respiratory Syncytial Virus
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: AU PO 0265
EARLIER PILING DATE: 1997-06-04
EARLIER FILING DATE: 1996-06-05
WUNBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Jeffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REPERBUCE: 415852000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILIG DATE: 1998-12-17
EARLIER APPLICATION NUMBER: PCT/AU97/00351
EARLIER FILING DATE: 1997-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.0%; Score 285; DB 16; Length 49; 98.0%; Pred. No. 2.3e-25;
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Pred. No. 2.3e-25;
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                Sequence 2, Application US/09202035 GENERAL INFORMATION:
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98.0%;
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Matches 48; Conserv
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Matches 48; Conserv
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LENGTH: 49
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                       1 KORQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
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OTHER INFORMATION: biotinyl amide derivativisation
FEATURE:
NAME/KEY: SITE
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100.0%; Pred. No. 6.1e-25;
iive 0; Mismatches 0;
                                                                                                                                                                                          APPLICANT: Jeffrey John Gorman
TITLE OF INVENTION: Viral Peptides with Structural
TITLE OF INVENTION: Wiral Peptides with Structural
FITLE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 415822000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: PGT/AU97/00351
EARLIER FILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 43
LENGTH: 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: PRT
ORGANISM: respiratory syncytial virus
                                                                                                                               US-09-202-035-43; Sequence 43, Application US/09202035; GENERAL INFORMATION:
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; OTHER INFORMATION: amidation
US-09-202-035-43
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Best Local Similarity 100.0
Matches 49; Conservative
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NAME/KEY: SITE
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LENGTH: 298
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Sequence 8, Application US/09202035

Sequence 8, Application US/09202035

GRNERAL INFORMATION:

TPLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of

TITLE OF INVENTION: Respiratory Syncytial Virus

FILE REPERENCE: 415852000100 NUMBER: US/09/202,035

CURRENT APPLICATION NUMBER: US/09/202,035

CURRENT FILING DATE: 1998-12-17

EARLIER APPLICATION NUMBER: AU PO 0265

EARLIER FILING DATE: 1996-06-05

NUMBER OF SEQ ID NOS: 44

SOFTWARE: Patentin Ver. 2.1
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US-09-647-308A-40

Sequence 40, Application US/09647309A

GENERAL INFORMATION:
APPLICANT: Pierre Fabre Medicament
FILE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY
FILE REFERENCE: D17064
CURRENT FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: FR 98 03814
PRIOR FILING DATE: 1998-03-27
NUMBER OF SEQ ID NOS: 136
SOFTWARE: Patentin Vers. 2.0
SEQ ID NO 40
LENTH: 59
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GENERAL INFORMATION
APPLICANT: Pierre Fabre Medicament
TITLE OF INVENTION: USE OF ACTIVE P40 CONJUGATES FOR NASAL DELIVERY
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                                                                1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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                      Indels
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  98.0%; Pred. No. 2.3e-25; tive 1; Mismatches 0;
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Pred. No. 2.3e-25;
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98.0%;
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Best Local Similarity 98.0°
Matches 48; Conservative
  Best Local Similarity 98.0
Matches 48; Conservative
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Best Local Similarity
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US-09-647-309A-38
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US-09-202-035-8
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GENERAL INFORMATION:
GENERAL INFORMATION:
TATLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
TITLE OF INVENTION: Respiratory Syncytial Virus
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REPREBENCE: 1989-12-17
CURRENT APPLICATION NUMBER: PCT/AU97/00351
EARLIER APPLICATION NUMBER: PCT/AU97/00351
EARLIER PILING DATE: 1996-06-05
NUMBER OF SEQ ID NOS: 44
SAGINARE: Patentin Ver. 2.1
SOFTWARE: Patentin Ver. 2.1
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GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Viral Peptides with Structural Homology to Protein G of
TITLE OF INVENTION: Respiratory Syncytial Virus
FILE REFERENCE: 415852000100
CURRENT APPLICATION NUMBER: US/09/202,035
CURRENT FILING DATE: 1998-12-17
EARLIER APPLICATION NUMBER: PCT/AU97/00351
EARLIER FILING DATE: 1997-06-04
EARLIER FILING DATE: 1997-06-05
NUMBER OF SEQ ID NOS: 44
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                  1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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Pred. No. 2.3e-25;
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                                                                                                                                                                                                             Score 285; DB 16;
Pred. No. 2.3e-25;
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                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
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EARLIER APPLICATION NUMBER: AU PO 0265
BARLIER FILING DATE: 1996-06-05
NUMBER OF SEG ID NOS: 44
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; ORGANISM: respiratory syncytial virus - US-09-202-035-6
                                                                                                                                                    ORGANISM: respiratory syncytial virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  respiratory syncytial virus
                                                                                                                                                                                                                99.0%;
98.0%;
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98.08;
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                                                                    SEQ ID NO 5
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US-09-202-035-7
                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
US-09-202-035-6
                                                                                                                                                                        us-09-202-035-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-202-035-7
                                                                                                                                                                                                                  Query Match
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Gaps

Search completed: November 22, 2002, 14:29:48 Job time : 142 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

November 22, 2002, 14:24:42; Search time 18 Seconds Run on:

(without alignments) 261.699 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-202-035-1 288 1 KQRQNKPPSKPNNDFHFEVF......NNPTCWAICKIPNKKPGKK

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	major surface qlyc	attachment protein	attachment protein	attachment protein	major surface glyc	G protein - Human	attachment protein	attachment protein	attachment protein	major surface glyc	surface		0	ď	glycoprotein G - b	glycoprotein G - o	attachment glycopr	diaminopimelate ep						diaminopimelate ep		charybdotoxin 1 [v	diaminopimelate ep		hypothetical prote
SUMMARIES	ΙD	MGNZ	JQ1205	JQ1204	JQ1208	MGNZRL	JC5680	JQ1207	JQ1206	JQ1209	MGNZ18	MGNZ60	MGNZBR	JQ2284	PQ0768	PQ0769	JQ2388	A48732	AE0468	AC0919	S01913	C91221	F86067	B60963	F64090	T13845	A60963	G82360	AD3432	A96808
	h DB	1 8						8																						
	Length	29	29	29	29	29	29	298	53	29	29	53	25	26	22	24	26	56	27	27	27	27	27	m	27	1861	m	29	375	150
dР	Query	100.0	99.0	99.0	0.66	0.66	0.66	97.2				0.99		27.8			26.9	26.9	23.1	23.1				22.2					21.2	21.0
	Score	288	285	285	285	285	285	280	279	273	190	190	83.5	80	79	77.5	77.5	77.5	66.5	66.5	66.5	66.5	66.5	64	63.5	63	62	62	61	60.5
	Result No.		7	რ	4	ស	9	7	ω	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

RESULT 2
JO1205
attachment protein - human respiratory syncytial virus (strain RSB1734)
N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1205
S;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. virol. 72, 2091-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: JQ1204; MUID:91374005; PMID:1895054
A;Molecule type: mRNA

neurotoxin Ts-kapp	diaminopimelate ep	diaminopimelate ep	hypothetical prote	probable protein k	diaminopimelate ep	probable E2F5 fami	hypothetical prote	gene el protein -	hypothetical prote	basic juvenile hor	T-cell surface gly	sex-specific stora	hypothetical prote	SYG1 protein - yea	signal peptidase I
S70473	G82986	T10459	T25507	T02584	C70458	G84775	A71822	S48861	T08663	B45046	150610	S01918	E82713	S49931	B84947
7	N	~	ď	~	7	~	~	N	~	~	7	7	~	7	7
57	276	276	518	176	279	532	792	1188	117	748	235	747	266	902	160
20.5	20.3	20.0	20.0	20.0	19.8	19.8	19.8	19.8	19.6	19.6	19.3	19.3	19.1	18.9	18.8
59	58.5	57.5	57.5	57.5	57	57	57	57	56.5	56.5	55.5	55.5	55	54.5	54
30	31	32	33	34	32	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1 MGNZ major surface glycoprotein G - human respiratory syncytial virus C;Species: human respiratory syncytial virus C;Species: human respiratory syncytial virus C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 24-Sep-1999 C;Accession: A94048; A93599; A04039 R;Wertz, G.W.; Collins, Prbry-Huang, X.,; Gruber, C.; Levine, S.; Ball, L.A.
Proc. Natl. Acad. Sci. U.S.A. 82, 4075-4079, 1985) A.Title: Nuclecitide Sequence of the G protein gene of human respiratory syncytial vir A.Title: Nuclecitide Sequence of the G protein gene of human respiratory syncytial vir A.Reference number: A94048; MUID:85216636; PMID:3858865 A.Reference type: mRNA A.Residues: 1-298 vMERA A.Residues: 1-298 vMERA A.Cross-references GR.W11486, GR.K01459, GR.K0719, GR.K013148, GR.K013149, GR.W11217;
7.1; PID: 933932 A;Note: residues 207-298 are identical with residues 376-467 of the nucleocapsid prot A;Note: this protein may carry 40.80 separate 0.1inked carbohydrate chains distribute R;Satake, M.; Coligan, J.E.; Elango, N.; Norrby, E.; Venkatesan, S. Nucleic Acids Res. 13, 7795-7812, 1985 A;Title: Respiratory syncytial virus envelope 91ycoprotein (G) has a novel structure.
A; Reference number: A93599; MUID: B006/198; PMID: 406999/ A; Accession: A93599 A; Accession: A93599 A; Residues: 1-298 <sat> A; Residues: 1-298 <sat> A; Cross-references: G8703149; NID: 960997; PIDN: CAA26928.1; PID: 960998 C; Superfamily: respiratory syncytial virus major surface glycoprotein G C; Keywords: glycoprotein; transmembrane protein F; 38-66/Domain: transmembrane #status predicted <tnm> F; 85, 135, 237, 251/Binding site: carbohydrate (Asn) (covalent) #status predicted</tnm></sat></sat>
 Query Match 100.0%; Score 288; DB 1; Length 298; Best Local Similarity 100.0%; Pred. No. 1.7e-26; Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy .1 KQRQNKPPSKPNNDFHFEVFNFVPCSTCSNNPTCWALCKRIPNKKPGKK 49

neutraliza

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Gaps

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Gaps

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G protein - Human respiratory syncytial virus

C species: Human respiratory syncytial virus

C; Species: J virol. 12, 317-322, 1996

A; Title: Molecular analysis of G protein gene of a respiratory syncytial virus strain

A; Reference number: JC5680

A; Reference number: JC5680

A; Reference number: JC5680

A; Residues: 1-298 <GEN>

A; Residues: 1-298 <GEN>

A; Residues: 1-298 <GEN>

A; Residues: 1-298 <GEN>

A; Roperimental source: strain B79

A; Note: the authors translated the codon TTT for residue 165 and 170 as Glu, TTC for C; Superfamily: respiratory syncytial virus major surface glycoprotein G

F; 1-38/Domain: intracellular #status predicted <IRM>

F; 39-66/Domain: transmembrane #status predicted <IRM>

F; 39-66/Domain: transmembrane #status predicted <IRM>

F; 39-66/Domain: Aransmembrane #status predicted <IRM

F; 39-66/Domain: Aransm
                                                                                                                                          C;Species: human respiratory syncytial testimatery syncytial testimatery syncytial testimatery syncytial testimatery syncytial states. 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999 C;Accession: A32703; S12279 S;Johnston, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L. Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987 A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A;Reference number: A32703; MUID:87289657; PMID:2441388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Residues: 1-298 (GAR>
C; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Keywords: glycoprotein; transmembrane protein
F; 41-63/Domain: transmembrane #status predicted <TMN>
F; 85,103,135,179,237,250,251,273,294/Binding site: carbohydrate (Asn) (covalent) #st-
                                                                                                                      respiratory syncytial virus (strain Long)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     attachment protein - human respiratory syncytial virus (strain RSB6190)
N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: J01207
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Accession: A32703
A,Molecule type: mRNA
A,Rolecule type: mRNA
A,Rolecule type: MRNA
A,Rossidues: 1-298 «JOH»
A,Cross-references: GB:M17212; NID:g333940; PIDN:AAA47411.1; PID:g333941
A,Gross-references: GB:M17212; NID:g333940; PIDN:AAA47411.1; PID:g333941
EMBO J: 9, 4181-4187; 1990
A,Title: Frame shift mutations as a novel mechanism for the generation of a
A,Reference number: S12279; MUID:91065351; PMID:2249671
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 285; DB 1;
Pred. No. 3.9e-26;
1; Mismatches 0
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                                                                                                                          G - human
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                                                                                                                          major surface glycoprotein
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Matches 48; Conserv
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A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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J. Gen. Virol. 72, 2091-2096, 1991
A.Ritier Identification of variable domains of the attachment (G) protein of subgroup A.R. Reference number: J01204, MUID:91374005; PMID:1895054
A.R. Residues: 1-297 CANNA
A.R. Residues: 1-297 CANNA
A.R. Residues: 1-297 CANNA
C.C. Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract illidren and daults.
C. Superfamily: respiratory syncytial virus major surface glycoprotein G
C.K. Reywords: glycoprotein, transmembrane protein
F. 85, 103, 135, 237, 251, 273, 294/Binding site: carbohydrate (Asn) (covalent) #status predict
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                                                                 ildren and adults.
C;Superfamily: respiratory syncytial virus major surface glycoprotein G
C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
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C;Keywords: glycoprotein; transmembrane protein
F;85,103,135,144,237,273/Binding site: carbohydrate (Asn) (covalent) #status predicted
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J. Geni, Virol. 72, 2001-2096, 1991
A;Title: Identification of variable domains of the attachment (G) protein of subgroup
A;Reference number: JQ1204; MUID:91374005; PMID:1895054
                                        Respiratory syncytial virus commonly causes severe lower respiratory tract
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A; Molecule type: mRNA
A; Residues: 1-297 <CAN>
C; Comment: Respiratory syncytial virus commonly causes severe lower respiratory ildren and adults.
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N;Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: JQ1208
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                                                                                                                                                                                                                                                                        Score 285; DB 2; Length 297;
Pred. No. 3.9e-26;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 297;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKR 197
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Pred. No. 3.9e-26,
1; Mismatches 0, Indels
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Pred. No. 3.9e-26;
1; Mismatches 0; Indels
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98.0%;
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Local Similarity 98.0%;
les 48; Conservative
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ilarity 98.0%;
Conservative
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Best, Local Similarity
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Best Local Similarity
A; Residues: 1-297
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Matches
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Gaps

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C;Accession: B32703
R;Johnson, P.R.; Spriggs, M.K.; Olmsted, R.A.; Collins, P.L.
Proc. Natl. Acad. Sci. U.S.A. 84, 5625-5629, 1987
A;Title: The G glycoprotein of human respiratory syncytial viruses of subgroups A and A;Reference number: A32703; MUID:87289657; PMID:2441388
A;Accession: B32703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             major surface glycoprotein G - human respiratory syncytial virus (strain 8/60)
N.Alternate names: attachment glycoprotein G
C.Species: human respiratory syncytial virus
C.Species: human respiratory syncytial virus
C.Sacession: A3707
R.Sullender, W.M.; Anderson, K.; Wertz, G.W.
Virology 178, 195-203, 1990
A.Title: The respiratory syncytial virus subgroup B attachment glycoprotein: analysis gous subgroup virus challenge.
A.Reference number: A37077; MUID:90357765; PMID:1697126
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S.Reywords: glycoprotein; transmembrane protein
F.45-63/Domain: transmembrane #status predicted <TMN>
F.91.86,100,230,290/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                     major surface glycoprotein G - human respiratory syncytial virus (strain 18537)
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:M55633; NID:g333944; PIDN:AAA47413.1; PID:g333945 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA

A; Residues: 1-292 < COGHS

A; Residues: 1-292 < COGHS

A; Cross-references: GB: M17213; NID: g333942; PIDN: AAA47412.1; PID: g333943

C; Superfamily: respiratory syncytial virus major surface glycoprotein G

C; Superfamily: respiratory syncytial virus major surface glycoprotein G

C; Keywords: glycoprotein; transmembrane protein

E; 41.63/Domain: transmembrane #status predicted <TMN>

F; 81, 86, 100/Painding site: carbohydrate (Asn) (covalent) #status predicted
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Pred. No. 5.7e-15;
4; Mismatches 13; Indels
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                                                                       149 KSRSKNPPKKPKDDYHFEVFNFVPCSICGNNQLCKSICKTIPSNKPKKK 197
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                2; Indels
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Pred. No. 5.7e-15;
4; Mismatches 13;
                Mismatches
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Best Local Similarity 65.3%;
Matches 32; Conservative
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Best Local Similarity 65.3%;
Matches 32; Conservative
                Conservative
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A; Molecule type: mRNA
A; Residues: 1-292 <SUL>
                46;
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MGNZ60
                   Matches
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C.Species: human respiratory syncytial virus
C.Species: human respiratory syncytial virus
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C.Accession: J01209
C.Accession: J01209
C.Accession: J01209
A.Title: Identification of variable domains of the attachment (G) protein of subgroup P.A.Title: Identification of variable domains of the attachment (G) protein of subgroup P.A.Reference number: J01209
A.Accession: J01209
A.Accession: J01209
A.Residues: 1-297 <CAN>
C.Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract: er children and adults.
C.Superfamily: respiratory syncytial virus major surface glycoprotein G
C.Superfamily: respiratory syncytial virus major surface glycoprotein G
C.Superfamily: J35,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predic
J. Gen. Virol. 72, 2091-2096, 1991
A.Title: Identification of variable domains of the attachment (G) protein of subgroup A.Reference number: J01204; MUID: 91374005; PMID: 1895054
A.Accession: J0207
A.Molecule type: mRNA
A.Rolecule type: mRNA
A.Note: the authors translated the codon ACC for residue 4 as Asn and AGC for residue C.Comment: Respiratory syncytial virus commonly causes severe lower respiratory traction and adults.
C.Superfamily: respiratory syncytial virus major surface glycoprotein G
C.Keywords: glycoprotein; transmembrane protein
F:85,103,135,237,250,273,294/Binding site: carbohydrate (Asn) (covalent) #status predic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                attachment protein - human respiratory syncytial virus (strain RSB5857)

N.Alternate names: G protein
C;Species: human respiratory syncytial virus
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Feb-1997
C;Accession: J01206
R;Cane, P.A.; Matthews, D.A.; Pringle, C.R.
J. Gen. Virol. 72, 2031-2036, 1991
A;Tille: Identification of variable domains of the attachment (G) protein of subgroup A;Reference number: J01204; MUID:91374005; PMID:1895054
A;Accession: J01206
A;Molecule type: mRNA
A;Residues: 1-297 cCAN>
C;Comment: Respiratory syncytial virus commonly causes severe lower respiratory tract ildren and adults.
C;Superfamily: respiratory syncytial virus major surface glycoprotein G;Keywords: glycoprotein; transmembrane protein
F;85,103,135,237,251,273,294/Binding site: carbohydrate (Asn) (covalent) #status predi
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N;Alternate names: G protein
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Pred. No. 2e-25;
1; Mismatches 1; Indels
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Pred. No. 1.5e-25;
2; Mismatches 0;
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Pred. No. 1e-24;
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93.9%;
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Best Local Similarity 95.9%;
Matches 47; Conservative
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ilarity 95.9%;
Conservative
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les 47; Conserv
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Best Local Similarity
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Best Local Si
Matches 47;
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Search completed: November 22, 2002, 14:26:59 Job time: 19 secs
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                               R;Lerch, R.A.; Anderson, K.; Wertz, G.W.
J. Virol. 64, 5559–5569, 1990
A;Title: Nucleotide sequence analysis and expression from recombinant vectors demonstrat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Mallipeddi, S.K.; Samal, S.K.
J. Gen. Virol. 74, 2001-2004, 1993
A;Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial
A;Reference number: JQ2284; MUID:93389461; PMID:8376974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G; Species: bovine respiratory syncytial virus
C; Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C; Accession: PQ0768
R; Mallipeddi, S. K.; Samal, S. K.
J. Genl Virol. 74, 2001-2004, 1993
A; Title: Sequence variability of the glycoprotein gene of bovine respiratory syncytial A; Reference number: JQ2284; MUID:9389461; PMID:8376974
A; Accession: PQ0768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F;45-62/Domain: transmembrane *status predicted <TMN>
F;3,85,127,149,233,251/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A) Residues: 1-263 - (MAL)
A) Experimental Source: isolate A51908
A) Experimental source: isolate A51908
C) Superfamily: respiratory syncytial virus major surface glycoprotein G
C) Superfamily: respiratory syncytial virus major surface glycoprotein G
C) Superfamily: ransmembrane protein
F) 1-38 (Domain: intracellular #status predicted <CYT>
F) 39-66 (Domain: extracellular #status predicted <EXT>
F) 67-263 (Domain: extracellular #status predicted <EXT>
F) 177,163,251/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein G - bovine respiratory syncytial virus (isolate A51908)
C;Species: bovine respiratory syncytial virus
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
C;Accession: J02284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                          A; Cross-references: GB: M58307; NID: 9210830; PIDN: AAA42810.1; PID: 9210831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Molecule type: mRNA

A.Molecule type: MAL>

C.Superfamily: respiratory syncytial virus major surface glycoprotein G

C.Superfamily: respiratory syncytial virus major surface glycoprotein G

C.Keywords: glycoprotein; transmembrane protein

F:1-31/Domain: intracellular #status predicted <INT>

F;32-59/Domain: transmembrane #status predicted <INM>
                                                                                                                                                                                                                                                                                                                                                                                                          C; Superfamily: respiratory syncytial virus major surface glycoprotein C; Keywords: glycoprotein; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6 KPPSKPNNDF-----HFEVFNFVPCSICSNNPTCWAIC----KRIPNKKP 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.0%; Score 83.5; DB 1; Length 25
29.6%; Pred. No. 0.017;
ive 9; Mismatches 16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / Match 27.8%; Score 80; DB 2; Length 263. Local Similarity 29.8%; Pred. No. 0.044; nes 14; Conservative 9; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 QNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAIC----KRIPNKKP 46
                                                                                                                                   y syncytial virus.
A;Reference number: A36408; MUID:91012801; PMID:2214024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similaricy
hes 16; Conservative
                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-257 < LER>
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A; Molecule type: mRNA
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C; Accession: A36408
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A Accession: P00769
A; Molecule type: mRNA
A; Restance: 1248 cMALA
A; Molecule type: mRNA
A; Respignes: 1248 cMALA
A; Molecule type: mRNA
A; Respectimental source: isolate VC464
A; Note: the authors translated the codon ACC for residue 85 as His and ATC for residue 5; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Superfamily: respiratory syncytial virus major surface glycoprotein G
C; Superfamily: transmembrane protein
F; 1-29/Domain: intracellular #status predicted <INT>
F; 1-29/Domain: transmembrane #status predicted <INT>
F; 18-348/Domain: extracellular #status predicted <IXT>
F; 76,154,224,242/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of bovine respiratory syncytim
F;60-250/Domain: extracellular #status predicted <EXT>
F;78,156,226,241,244/Binding site: carbohydrate (Asn) (covalent) #status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           olycoprotein G - bovine respiratory syncytial virus (isolate VC464) (fragment) C;Species: bovine respiratory syncytial virus C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 07-May-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 26.9%; Score 77.5; DB 2; Length 248; Best Local Similarity 30.8%; Pred. No. 0.081; Matches 16; Conservative 8; Mismatches 19; Indels
                                                                                                                      Query Match 27.4%; Score 79; DB 2; Length 250; Best Local Similarity 26.7%; Pred. No. 0.055; Matches 12; Conservative 11; Mismatches 22; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 KPPSKP-----NNDFH--FEVFNFVPCSICSNNPTCWAICKRIPNKKPGK
                                                                                                                                                                                                                                                                                                                                                  4 QNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGK 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: PQ0769
R; Mallipeddi, S. K.; Samal, S.K.
J. Gen. Virol. 74, 2001–2004, 1993
A; Title: Sequence variability of the glycoprotein gene of A; Reference number: JQ2284; MUID:93389461; PMID:8376974
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

November 22, 2002, 14:17:16; Search time 11 Seconds Run on:

(without alignments) 184.758 Million cell updates/sec

Title: Perfect score: Sequence:

US-09-202-035-1 288 1 KQRQNKPPSKPNNDFHFEVF......NNPTCWAICKRIPNKKPGKK 49

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 Total number of hits satisfying chosen parameters: 112892 seqs, 41476328 residues Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	P03423 human respi	human	human	human	5 human	4 human	human	human	human	human	bovine	bovine	bovine	7 bovine	_	3 bovine	34	bovine	Q84183 bovine resp	bovine	pasteur	_	_		7 yersinia		59 haemoph	P13487 leturus qui	vibrio o	Q9nii6 mesobuthus	10	322	O67693 aquifex aeo
SUMMARIES	ព	VGLG_HRSVA	VGLG_HRSV2	VGLG_HRSV3	VGLG_HRSV6	VGLG_HRSVL	VGLG_HRSV5	VGLG_HRSV4	VGLG_HRSV7	VGLG_HRSV1	VGLG_HRSV8	VGLG_BRSVC	VGLG_BRSV2	VGLG_BRSVS	VGLG_BRSVW	VGLG_ORSVW	VGLG_BRSV1	VGLG_BRSV4	VGLG_BRSVL	VGLG_BRSVR	VGLG_BRSV7	DAPF_PASMU	DAPF_ECO57	DAPF_ECOLI	DAPF_SALTY	DAPF_YERPE	SCK2_LEIQH	DAPF_HAEIN		DAPF_VIBCH			DAPF_PSEFL	DAPF_AQUAE
	Length DB	298 1	297 1			298 1						257 1								257 1											57 1		276 1	279 1
ø	Query Match	100.0	99.0	99.0	0.66	0.66	97.2	96.9	94.8	0.99	99	29.0	27.8	26.9	26.9	26.9	26.6	26.6	25.7	25.7	25.3	23.4	23.1	23.1	23.1	23.1	22.2	22.0	┥	а.	21.0	0	20.0	19.8
	Score	288	285	285	285	285	280	279	273	190	190	83.5	80	77.5	77.5	77.5	76.5	76.5	74	74	73	67.5	99.3	66.5	66.5	66.5	64	63.5	62		60.5	œ	57.5	57
	Result No.	-	73	m	4	Ŋ	ø	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	38	29	30	31	32	33

Q06342 trichoplusi P09179 bombyx mori P50219 tityus serr Q9n115 mesobuthus P40528 saccharomyc Q9k1v1 heamophilus P57248 buchnera ap P97436 mus musculu P57649 buchnera ap P34878 lactococcus P11332 european el P25118 mus musculu
JSB1_TRINI SSP1_BOMMO SCK_TITSE SCK_TITSE SCK_TITSE SCK_TEAN SVG1_YEAST HGBB_HAEIN LSPA_BUCAI HK31_MOUSE MTSB_LACLC VET_PAPVE TRIA_MOUSE
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748 747 35 58 902 1067 1460 237 284 360 1102
199.06 118.09 118.09 118.09 118.09 118.00 119.00
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4668993333333333333333333333333333333333

ALIGNMENTS

	GCCCCCCCCCFFFFFFFFFFFFFFFFFFFFFFFFFFFF	RESULT 1 VOLCE, HRSVA TO T	
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NCBI_TaxID=11253;
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P27025;
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                                                                                                                                VGLG_HRSV3
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                                                                                                              VGLG_HRSV3
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A Cane P.A. Matthews D.A., Pringle C.R.;
Cane P.A. Matthews D.A., Pringle C.R.;
Cane P.A. Matthews D.A., Pringle C.R.;

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dified and this statement is not removed. Usage by and for commercial tities requires a license agreement (See http://www.isb-sib.ch/announce/send an email to license@lsb-sib.ch).
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                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

993C3D2DD68BC634 CRC64;
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                               Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     149 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human respiratory syncytial virus (strain rsb642).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID-11252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FC72A7F3A8EBF67C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 288; DB 1; 100.0%; Pred. No. 6.9e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                               EMBL; uosur.,
PIR; Ad4039; MGNZ.
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
Pfam; PF00802; Glycoprotein.
CYTO CYTO
                                                                                                                                                                                                                                                                                                                                             32586 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32745 MW;
                                                                     EMBL; M11486; AAB59857.1; -. EMBL; X03149; CAA26928.1; -. EMBL; U50362; AAB86663.1; -. EMBL; U50363; AAB86675.1; -. EMBL; U63644; AAC55969.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                  49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                    38
67
135
135
237
251
251
298 AA;
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135
144
144
237
297 AA;
                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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P27021;
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MEDLINE-91374005; PubMed=1895054;
MEDLINE-91374005; PubMed=1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).
-: FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTTAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
-: SUBCELLUAR LOCATION: EXPERSSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-: PTM: MAY CARRY 40-80 SEBRARE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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MEDLINE-91344005; PubMed-1895054;
MEDLINE-91344005; PubMed-1895054;
MEDLINE-91344005; PubMed-1895054;
"Iden P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 72:2091-2096(1991).
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N-LINKED (GLCNAC. .) (POTENTIAL).
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                     149 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKR 197
KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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Pred. No. 1.5e-26;
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                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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                                                                                                                                                                                                   01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein
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                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus (strain rsb1734)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus (strain rsb6256)
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01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
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98.0%; Pred. No. 1...
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InterPro; PRR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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297 AA;
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Best Local Similarity
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POTENTIAL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                    Gaps
                                       -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-1- PTM: MAY CARRY 40-08 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
INTERPO: IPROUGUS; Glycoprot_G.
Pfam: PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRARM OF THE VIRIONS.
-1- PTM: MAY CARRY 40-460 SEPRATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
6781756C38B64A80 CRC64;
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Viruses; SSRA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11260;
                                                                                                                                                                                                                                                                                                      Score 285; DB 1; Length 297; Pred. No. 1.5e-26;
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                                                                                                                                                                                    EXTRACELLULAR (POTENTIAL)
                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
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01-FEB-1996 (Rel. 33, Last sequence update)
01-FEB-1996 (Rel. 33, Last annotation updat
                                                                                                                                                                                                                                                                                                                                 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR; A32703; MGNZRL.
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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297
103
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67
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297 AA;
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P20895;
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     subgroup A respiratory syncytial viruses.";
J. Gen. Virol. 77:2091-2096(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-!- PTM: MAY CARRY 40-80 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
         EXTRACELLULAR (POTENTIAL).
N-LINKED (GLCNAC. ...) (POTENTIAL).
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11255;
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                                                                                                     B79FEFA4B4A73B0E CRC64;
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(Rel. 23, Last sequence update)
(Rel. 39, Last annotation update)
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cane P.A., Matthews D.A., Pringle C.R.; "Identification of variable domains of t
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MEDLINE=91374005; Pubmed-1895054;
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InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; l.
Transmembrane; Glycoprotein.
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98.0%;
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                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                          STANDARD;
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298 AA;
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01-AUG-1992 (
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P27024;
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P27023;
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VGLG_HRSV5
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llarity 93.9%;
Conservative
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tes 46; Conserv
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P20896;
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SEQUENCE
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CARBOHYD
                                                                                                            TRANSMEM
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                                                                                            DOMAIN
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     HIDDER KENTER FERTER FOR SOLUTION OF SOLUT
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                                                                                                                                                                                                                                             MEDLINE-91374005; PubMed-1895054;

Cane P.A., Matthews D.A., Pringle C.R.;

Cane P.A., Matthews D.A., Pringle C.R.;

Identification of variable domains of the attachment (G) protein of subgroup A respiratory syncytial viruses.";

J. Gen. Virol. 72:2091-2096(1991).

I. Gen. Virol. 72:2091-2096(1991).

RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.

SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.

CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-91374005; PubMed-1895054;
Cane P.A., Matthews D.A., Pringle C.R.;
"Identification of variable domains of the attachment (G) protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 297; 7.8e-26; thes 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus (strain rsb6614).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                       Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32772 MW; 10488CCA475936BE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Major surface glycoprotein G (Attachment glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                      Human respiratory syncytial virus (strain rsb5857)
01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
01-AUG-1992 (Rel. 23, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66
297
85
103
135
237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-11257;
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P27026;
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TRANSMEM
DOMAIN
CARBOHYD
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CARBOHYD
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87289657; PubMed=2441388; Med., Collins P.L.; Johnson P.R., Spridgs M.K., Olmsted R.A., Collins P.L.; The G glycoprotein of human respiratory syncytial viruses of subgroups A and B: extensive sequence divergence between antigenically related proteins."; Proc. Natl. Acad. Sci. U.S., 84:5625-5629(1987).

-I- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRAND OF THE VIRIONS.
-i- PTM: MAY CARRY 40-40 SEPARATE O-LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
58B384028E437ACD CRC64;
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N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

N-LINKED (GLCNAC. . ) (POTENTIAL).

BC8CS9F69CA7AFC2 CRC64;
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Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
VCBI_TaxID-11251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 273; DB 1; Length 297;
Pred. No. 4e-25;
DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149 KQHQNKPPNKPNHFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1991 (Rel. 17, Created)
01-REB-1991 (Rel. 17, Last sequence update)
01-RNOY-1991 (Rel. 20, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2; Indels
                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).
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1; Mismatches
                                                                                                                                                                                                                                       POTENTIAL.
                                  PIR; J01209; J01209.
InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000925; Glycoprot_G. Pfam; PF00802; Glycoprotein_G; I. Transmembrane; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sullender W.M., Mufson M.M., Anderson L.J., Wertz G.W.;
"Genetic diversity of the attachment protein of subgroup B
respiratory syncytial viruses.";
J. Virol. 65:5425-5434(1991).
-!- FUNCTION: UNLIKE THE OTHER PARAWXXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sullender W.M., Anderson K., Wertz G.W.;
"The respiratory syncytial virus subgroup B attachment glycoprotein:
analysis of sequence, expression from a recombinant vector, and
evaluation as an immunogen against homologous and heterologous
subgroup virus challenge.";
                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -1- SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE WEMBRANG OF THE VIRIONS.
-1- PTM: MAY CARRY 40-96 SEPARATE O'LINKED CARBOHYDRATE CHAINS DISTRIBUTED AMONG THE 91 SERINE AND THREONINE RESIDUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).

8EC60C85EF057BB5 CRC64;
                                     ;
                                                                                                                                                                                                                                                                                                                   Human respiratory syncytial virus (subgroup B / strain 8/60).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11258;
   Length 292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 292;
                                                                                         149 KSRSKNPPKKPKDDYHFEVFNFVPCSICGNNQLCKSICKTIPSNKPKKK 197
                                                                      1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                     13; Indels
                                                                                                                                                                                                                                                                                         Major surface glycoprotein G (Attachment glycoprotein G)
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Pred. No. 2.2e-15;
4; Mismatches 13;
 Score 190; DB 1;
Pred. No. 2.2e-15;
4; Mismatches 13
                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-90357765; PubMed-1697126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE-91374595; Pubmed-1895391;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000925; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
                                                                                                                                                                                                                             01-NOV-1991 (Rel. 20, Created)
01-NOV-1991 (Rel. 20, Last seq
01-AUG-1992 (Rel. 23, Last anno
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292 E3
81 N.
86
100
32143 MW;
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65.3%;
 65.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            subgroup virus challenge."; Virology 178:195-203(1990).
Query Match
Best Local Similarity 65.3
Matches 32; Conservative
                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A37077; MGNZ60.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transmembrane;
                                                                                                                                                                                                VGLG_HRSV8
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TRANSMEM
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Gaps

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13; Indels

Conservative

32;

Best Loca Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=91012801; PubMed=2214024;
Lerch R.A., Anderson K., Wertz G.W.;
Lerch R.A., advence analysis and expression from recombinant vectors demonstrate that the attachment protein G of bovine respiratory syncytial virus is distinct from that of human respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i-SUBCELLUIAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
-i-SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                Bovine respiratory syncytial virus (strain Copenhagen) (BRS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97098087; PubMed=8942628;
Doredeijers J.F., Langedijk J.P.M., Haard K., Boelens R.,
Rullmann J.A., Schaaper W.M., van Oirschot J.T., Kaptein R.;
"Solution structure of the immunodominant region of protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 83.5; DB 1; Length 257;
Pred. No. 0.0063;
9; Mismatches 16; Indels 13
                  149 KSRSKNPPKKPKDDYHFEVFNFVPCSICGNNQLCKSICKTIPSNKPKKK 197
49
                                                                                                                                                                                                 Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                                                                                                                                                Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
 1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OB86D541FBA0657D CRC64;
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                                                                                                                                                                                  annotation update)
                                                                                                                                                                 Last sequence update)
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Glycoprotein; 3D-structure.
                                                                                                                 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bovine respiratory syncytial virus.";
Biochemistry 35:14684-14688(1996).
                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; A36408; MGNZBR.
PDB; 1BRV; O5-JUN-97.
Interpro; IRYCO0092; Glycoprot_G.
Pfam; PF00802; Glycoprotein_G; 1.
                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last seq
15-JUL-1998 (Rel. 36, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                    J. Virol. 64:5559-5569(1990).
[2]
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251
257 AA;
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Matches 16; Conserv
                                                                                                                                                                                                                                                                                  NCBI_TaxID=11248;
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HRS VIRUS.
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Best Local Simi
Matches 16;
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O10687;
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                                                                                                                                                                                                                                                                                   RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND HEMAGGLUTINATING ACTIVITIES.
                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-97288324; PubMed-9143302;
Furze J., Roberts S., Wertz G., Taylor G.;
Antigenically distinct G glycoproteins of BRSV strains share a high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRUS.
                                                                                                                                                                                                                                                  degree of genetic homogeneity.";
Virology 231:48-58(1997).
1- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS,
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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27.8%; Score 80; DB 1; Length 263; 29.8%; Pred. No. 0.017;
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G).
                                                                                                                              Major surface glycoprotein G (Attachment glycoprotein G)
                                                                                                                                                    Bovine respiratory syncytial virus (strain 220-60) (BRS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
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A630883D51ED02D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                            (5-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
                                                                          263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     257 AA
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Pfam; PF00802; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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263 EX
186 BY
182 BY
1127 N-
163 N-
251 N-
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173
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263 AA;
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                                                                          VGLG_BRSV2
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010686;
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TRANSMEM
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CARBOHYD
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CARBOHYD
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                                                              VGLG_BRSV2
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                                                                                                                                                                                                                                                               degree of genetic homogeneity.";
Virology 231:48-58(1997).
-!- FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE
RESPIRATORY SYNOYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
HEMAGGLUTINATING ACTIVITIES.
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Furze J., Roberts S., Wertz G., Taylor G.;
"Antigenically distinct G glycoproteins of BRSV strains share a high
degree of genetic homogeneity.";
Virology 231:48-58(1997).
                                                                                                                                                                         MEDLINE-97288324; PubMed-9143302;
Furze J., Roberts S., Wertz G., Taylor G.;
"Antigenically distinct G glycoproteins of BRSV strains share a high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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-1- SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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Pred. No. 0.032;
8; Mismatches 19; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
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Bovine respiratory syncytial virus (strain Snook) (BRS).
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Major surface glycoprotein G (Attachment glycoprotein G)
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=82825;
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ilarity 30.8%;
Conservative
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257 AA;
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SEQUENCE
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                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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FUNCTION: UNLIKE THE OTHER PARAMYXOVIRUS ATTACHMENT PROTEINS, THE RESPIRATORY SYNCYTIAL VIRUS G PROTEIN LACKS BOTH NEURAMINIDASE AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 KPPSKP-----NNDFH--FEVFNFVPCSICSNNPTCWAIC------KR 40
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                               HEMAGGIUTINATING ACTIVITIES.
SUBCELLULAR LOCATION: EXPRESSED ON THE SURFACE OF THE INFECTED CELLS AND INCORPORATED IN THE MEMBRANE OF THE VIRIONS.
SIMILARITY: TO THE G PROTEINS OF EITHER THE SUBGROUP A OR B HRS VIRIOS.
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N-LINKED GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26.9%; Score 77.5; DB 1; Length 263; 29.0%; Pred. No. 0.033; 1ve 5; Mismatches 19; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Major surface glycoprotein G (Attachment glycoprotein G).
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EXTRACELLULAR (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
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15-JUL-1998 (Rel. 36, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update
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                                                                                                                                                                                                                                                                                                                                                                   HSSP; P22261; 1BRV.
InterPro: PPR00025; Glycoprot_G.
Pfam; PF006002; Glycoprotein_G; 1.
Transmembrane; Glycoprotein.
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                                                                                                                                                                                                                                                                                                                                          EMBL; Y08717; CAA69967.1; -.
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Matches 20; Conservative
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086695;
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce.or send an email to license@lsb-sib.ch)
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EXTRACELULAR (POTENTIAL).

BY SIMILARITY.

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N-LINKED (GLCNAC. .) (POTENTIAL).

N-LINKED (GLCNAC. .) (POTENTIAL).
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25.8%; Pred. No. 0.033;
tive 10; Mismatches 1
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Job time : 12 secs
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EMBL; S67862; AAB29551.1; JOINED.
HSSP; P22261; 1BRV.
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Matches 17; Conservative
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"Antigenic and genetic diversity among the attachment proteins of group A resplratory syncytial viruses that have caused repeat infections in children.";
J. Infect. Dis. 178:925-932(1998).
EMBL; AF065407; AAD02943.1;
InterPro; IPR000925; Glycoprot_G.
InterPro; IPR003880; Ppantne_attach.
InterPro; IPR002880; Ppantne_attach.
InterPro; IPR002965; P.rich_extensn.
PRINTS; PR01217; PRICHEXTENSN.
PRINTS; PR01217; PRICHEXTENSN.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Attachment glycoprotein G (Fragment).
Human respiratory syncytial virus.
Viruses; ssRAA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
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SEQUENCE 293 AA; 32125 MW; 17B5B43396A63CCF CRC64;
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100.0%; Pred. No. 1.6e-31;
11ve 0; Mismatches 0;
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MEDLINE=99022964; PubMed=9806017;
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Genetic diversity and molecular epidemiology of the G protein of
subgroups A and B of respiratory syncytial virus isolated over 9
consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
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EMBL, FAI93312.; AAF23735.1; InterPro; IPR000925; Glycoprot_G. InterPro; IPR003880; Ppantne_attach. InterPro; IPR003880; Prich extensn.
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       Length 278;
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Viruses; sRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Viruses; sRNA negative-strand viruses; Mononegavirales;
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01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
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MEDLINE=20283719; Pubmed=10823752;
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   99.0%;
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Query Match
Best Local Similarity 98.0
Matches 48; Conservative
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A Choi E.H., Lee H.J.; Choi E.H., Ch
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"Genetic diversity and molecular epidemiology of the g protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556(2000).

MRL; AR193309; ARF23732.1;

InterPro; IPR00925; Glycoprot.G.

InterPro; IPR00926; Prich_extensn.

PRINTS; PR01217; PRICHETENSN.

PROSTIE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN.1.
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Pred. No. 3.8e-31;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBL_TaxID=11250;
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MEDLINE=20283719; PubMed=10823752;
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STRAIN=91242;
MEDLINE=20283719; PubMed=10823752;
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Best Local Similarity
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C STRAIN=94191;
MEDILINE=20283119; PubMed=10823752;
MEDILINE=20283119; PubMed=10823752;
A Choi E.H. Lee H.J.;
"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 ronsecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
RMBL, AR193316; AR23739.1; ...
RRBL, AR193316; AR23739.1; ...
InterPro: IPR000325; Glycoprot_G.
InterPro: IPR000386; Panthe_attach.
InterPro: IPR000365; Pinch_extensn.
RR Pf00802; Glycoprotin_G: IRRBL.
RR PF00802; Glycoprotin_G: IRRBL.
RR PF00802; Glycoprotein_G: IRRBL.
RR PF00802; Glycoprotein_G: IRRBL.
RR PRINTS; PR01217; PRICHEXTENSN.
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Pred. No. 3.8e-31;
1; Mismatches 0; Indels
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Pfam; PF00802; Glycoprotein_G; 1.
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PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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"Genetic diversity and molecular epidemiology of the G protein a subgroups A and B of respiratory syncytial virus isolated over sonsecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
BMBL; AF193307; AAF23730.1;
InterPro: IPR000925; Glycoprot_G.
InterPro: IPR000956; Prich_extensn.
InterPro: IPR0002965; Prich_extensn.
Prim; PR00802; Glycoprot_G.
INTERPROSECUTION PROFECUTION PR
Choi E.H., Lee H.J.;
"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
EMBL; AF193306; AAF23729.1;
InterPro; IPR000925; Glycoprot.G.
InterPro; IPR000808; Glycoprot.ac.
Pfam; PF00802; Glycoprotein.G: 1.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN.1.
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
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98.0%; Pred. No. 3.8e-31;
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98.0%; Pred. No. 3.8e-31;
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MEDLINE=20283719; PubMed=10823752;
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Choi E.H., Lee H.J.;
"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
BRME, AF193314, AF23737.1;
InterPro; IPR00925; Glycoprot.G.
InterPro; IPR00925; Prich.extensn.
InterPro; IPR00926; Prich.extensn.
PRIMTS; PR01217; PRIGETENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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BDLINE-20283719; PubMed-10823752;
Choi E.H., Lee H.J.;
"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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Pred. No. 3.8e-31;
1; Mismatches 0;
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PROSITE; PSO012; PHOSPHOPANTETHEINE; UNKNOWN_1.
NON_TER 1 1 SEQUENCE 279 AA; 30529 MW; AEC4D787983D472D
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01-MAY-2000 (TrEMBLRE1. 13, Last seq
01-MAR-2002 (TrEMBLRE1. 20, Last anno
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J. Infect. Dis. 181:1547-1556(2000).
EMBL; AF193317; AAF23740.1; -.
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InterPro; IPR003880; Ppantne_attach.
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Best Local Similarity 98.0%;
Matches 48; Conservative
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Gloetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.",
J. Infect. Dis. 181:1547-1556(2000).
EMBL; AF193308; AAF2373.1.;
InterPro; IPR009255; Glycoprot_G.
InterPro; IPR00880; ppantne_attach.
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"Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:1547-1556(2000).
EMBL; AF193311; AAF23734.1;
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
                                                     Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NGBI_TaxID=11250;
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PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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Pred. No. 3.8e-31;
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PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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InterPro; IPR002965; P_rich_extensn.
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MEDLINE=20283719; PubMed=10823752;
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        InterPro; IPR000225; Glycoprot_G.
InterPro; IPR003880; Ppantne_attach.
InterPro; IPR002965; P_ich_extensn.
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PRINTS; PR01217; PRICHEXTENSN.
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EMBL; AF193320; AAF23743.1; -
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Choi E.H., Lee H.J.;
Choi E.H., Lee H.J.;
Choi E.H., Lee H.J.;
Genetic diversity and molecular epidemiology of the G protein of subgroups A and B of respiratory syncytial virus isolated over 9 consecutive epidemics in Korea.";
J. Infect. Dis. 181:147-1556(2000).
EMBL; AF193319; AAF23742.1;
InterPro; IPR000255; Olycoprot.G.
InterPro; IPR003565; P.Isch.extensn.
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J. Infect. Dis. 181:1547-1556(2000).
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            Score 285; DB 12; Length 279;
Pred. No. 3.8e-31;
1; Mismatches 0; Indels (
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Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
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PRINTS; PR01217; PRICHEXTENSN.
PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.
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NCBI_TaxID=11250;
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            Query Match
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"Genetic diversity and molecular epidemiology of the G protein of a "Genetic diversity and molecular epidemiology of the G protein of subgroutive epidemics in Korea.";

J. Infect. Dis. 181:1547-1556(2000).

EMBL, AR193326, AAR23749.1;

InterPro: IPR0003880; Partch_attach.

InterPro: IPR0003880; Partch_attach.

InterPro: IPR002965; Prich_attach.

INTERPRO: IPR002965; Prich_attach.

RR PRINTS; PR01217; PRICHEXTENSN.

RR PRINTS; PR01217; PRICHEXTENSN.

RR PROSITE; PS00012; PHOSPHOPANTETHEINE; UNKNOWN_1.

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SEQUENCE 279 AA; 30467 MW; EAR3C99707A9DB47 CRC64;
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                                                                                                                                                                                       Human respiratory syncytial virus.
Viruses; ssRNA negative-strand viruses; Mononegavirales;
Paramyxoviridae; Pneumovirinae; Pneumovirus.
NCBI_TaxID=11250;
                                                  Created)
Last sequence update)
Last annotation update)
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PRT;
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                                                  (TrEMBLrel. 13, CTEMBLrel. 13, I (TrEMBLrel. 20, I
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PRELIMINARY;
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                       Compugen Ltd.
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compug
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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(cgn2_6/prodate/1/pubpaa/USOZ_OZ_PUBCOMB.pep:*

Sequence 20, Appl Sequence 18, Appl Sequence 27, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 11, Appl Sequence 181, App Sequence 28, Appl Sequence 20, Appl Sequence 48887, A Sequence 16, Appl 5081, A , Appli Sequence 35081 Sequence 30, Sequence 71, Sequence 71, Sequence 72, Sequence 72, Sequence 46, Sequence 2 Description 0 US-09-030-619-181 US-10-044-359-28 US-10-044-359-20 US-10-044-359-12 US-10-044-359-12 US-10-033-223-11 US-10-033-223-11 US-10-033-224-11 US-10-033-224-11 2 US-10-033-324-11 2 US-10-033-324-11 0 US-09-864-761-48887 US-10-044-359-16 US-09-9864-761-35081 US-09-879-257A-30 US-09-853-161-71 US-09-853-659A-71 US-09-726-643-46 US-09-726-643-46 SUMMARIES DB Query Match Length Score 62 56 53 51 51 51 51 51 51 50 50 50 Result Š.

Sequence 82, Appl	Sequence 1151, Ap	Sequence 34, Appl	Sequence 18, Appl	Sequence 11, Appl	Sequence 37986, A	Sequence 10, Appl	Sequence 6, Appli	Sequence 6, Appli	Sequence 418, App	Sequence 215, App	Seguence 15, Appl	Sequence 25, Appl	Sequence 15, Appl	Seguence 69, Appl	Seguence 949, App	Sequence 84, Appl	Sequence 44, Appl	Sequence 2, Appli	Seguence 2, Appli	Seguence 8, Appli	Sequence 13, Appl	Sequence 1, Appli	Sequence 22, Appl	Sequence 2, Appli	Sequence 40201, A
US-09-726-643-82	US-09-925-300-1151	US-10-016-283-34	US-09-989-903-18	US-09-854-864-11	US-09-864-761-37986	US-09-854-864-10	US-09-987-021-6	US-09-957-485-6	US-09-801-368-418	US-09-764-887-215	US-09-898-234-15	US-09-899-429A-25	US-09-899-422-15	US-09-888-615-69	US-09-764-869-949	US-09-801-574-84	US-09-908-805B-44	US-09-888-224-2	US-09-803-589-2	US-09-803-289-8	US-10-105-929-13	US-09-445-023A-1	US-09-801-574-22	US-10-105-929-2	US-09-864-761-40201
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17.2	17.2	17.2	17.0	16.8	16.8	16.8	16.8	16.8	16.8	16.7	16.7	16.7	16.7	16.7	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.5	16.3
49.5	49.5	49.5	49	48.5	48.5	48.5	48.5	48.5	48.5	48	48	48	48	48	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47.5	47
20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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GENERAL INFORMATION:
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Robert
APPLICANT: Taylor, Applicant Briles, Douglass
APPLICANT: Fraser, Janet R.
APPLICANT: West, Michael H.P.
APPLICANT: We
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 181
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US-10-044-359-28
Sequence 28, Application US/10044359
Sequence 28, Application US/10044359
GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
                                       Sequence 181, Application US/09030619B Patent No. US20020035061A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CSNNPTCWAICKRIPNKKPGK 48
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US-09-030-619-181
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                                                                                                                                                                                                                                                                                                                                                   Score 53; DB 9
Pred. No. 3.6;
5; Mismatches
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Pred. No. 3.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INCORACTION:
APPLICANT: Herman, Rafael
APPLICANT: Herman, Rafael
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT APPLICATION NUMBER: 09/599,416
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICROSOft Office 97
SEQ ID NO 27
LENGTH: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                PRIOR FILING DATE: 2000-06-22
PRIOR APPLICATION WUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 18
LENGTH: 58
  PRIOR APPLICATION NUMBER: 09/599,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 11, Application US/10033245
Patent No. US20020160392A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 5
US-10-044-359-27
; Sequence 27, Application US/10044359
; Patent No. US20020160454A1
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                                                                                                                                                                                                                                         Query Match 18.4%;
Best Local Similarity 27.8%;
Matches 10; Conservative 5
                                                                                                                                                                               ; ORGANISM: Hottentotta judaica US-10-044-359-18
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Best Local Similarity 33.3%;
Matches 7; Conservative
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Watanabe, Colin K.
Wood, William I.
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Gao, Wei-Qiang
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                                                                                                                                                              TYPE: PRT
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Pred. No. 2.7;
                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; Mismatches
            FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR APPLICATION NUMBER: 06/140,227
PRIOR PELING DATE: 1999-06-22
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WOOD, James F.
APPLICANT: WOOD, James F.
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR FILING DATE: 2000-06-22
PRIOR PELICATION NUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
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APPLICANT: Herrman, Rafael
APPLICANT: Wong, James F.
APPLICANT: Lee, Jian-Ming
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT APPLICATION NUMBER: US/10/044,359
CURRENT FILING DATE: 2002-01-11
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Sequence 20, Application US/10044359
Patent No. US20020160454A1
SEMERAL INFORMATION:
APPLICANT: Herrman, Rafael
TITLE OF INVENTION: SCORPION TOXINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/10044359 Patent No. US20020160454A1
                                                                                                                                                                                                                                                                                                                                                                                                   28 CSNNPTCWAICKRIPNKKPGK 48
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Best Local Similarity 38.1%;
Matches 8; Conservative
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33.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 28
SOFTWARE: Microsoft Office 97
SEQ ID NO 20
LENGTH: 57
                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Buthus martensii
US-10-044-359-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity 33.3
Matches 11; Conservative
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US-10-044-359-18
                                                                                                                                                                                               SEQ ID NO 28
LENGTH: 37
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPRENCE: 92010-12-7

CURREAT ABLICATION NUMBER: USA,003.23

CURREAT PALLAND DAVE: 2001-12-7

REIOR APPLICATION NUMBER: 60/13.415

REIOR APPLICATION NUMBER: 60/13.511

REIOR APPLICATION NUMBER: 60/13.511

REIOR APPLICATION NUMBER: 60/13.511

REIOR PELICATION NUMBER: 60/15.558

REIOR PELICATION NUMBER: 60/15.537

REIOR PELICATION NUMBER: 60/15.33

REIOR PELICATION NUMBER: 60/15.33

REIOR PELICATION NUMBER: 60/15.33

REIOR PELICATION NUMBER: 60/15.565

REIOR PELICATION NUMBER: 60/15.565

REIOR PELICATION NUMBER: 60/15.565

REIOR PELICATION NUMBER: 60/15.565

REIOR PELICATION NUMBER: 60/15.566

REIOR PELICATION NUMBER: PCT/US90/20564

REIOR PELICATION NUMBER: PCT/US90/20564

REIOR PELICATION NUMBER: PCT/US90/20565

REIOR PELICATION NUMBER: PCT/US90/20564

REIOR PELICATION NUMBER: PCT/US90/20566

REIOR PELINE DATE: 2000-00-30

REIOR PE
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                                                                                                                                                                            Pan, James
Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                     Watanabe, Colin K.
Wood, William I.
                      Ferrara, Napoleone
                                                                                 Gao,Wei-Qiang
Goddard,Audrey
Gurney,Austin L.
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; ORGANISM: Homo sapiens
US-10-033-223-11
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APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Pred. No. 38;
1; Mismatches 8; Indels
FILE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2930R1C7
CURRENT APPLICATION NUMBER: 05/095,325
PRIOR PELLING DATE: 1998-00-12-27
PRIOR PELLING DATE: 1998-12-16
PRIOR PELLOATION NUMBER: 60/113,511
PRIOR PELLOATION NUMBER: 60/115,586
PRIOR PELLOATION NUMBER: 60/115,586
PRIOR PELLOATION NUMBER: 60/115,333
PRIOR PELLOATION NUMBER: 60/119,341
PRIOR PELLOATION NUMBER: 60/119,341
PRIOR PELLOATION NUMBER: 60/110,331
PRIOR PELLOATION NUMBER: 60/110,331
PRIOR PELLOATION NUMBER: 60/110,362
PRIOR PELLOATION NUMBER: 60/110,362
PRIOR PELLOATION NUMBER: 60/110,362
PRIOR PELLOATION NUMBER: 60/10,262
PRIOR PELLOATION NUMBER: 60/100,303
PRIOR PELLOATION NUMBER: 60/100,303
PRIOR PELLOATION NUMBER: PCT/US99/1252
PRIOR PELLOATION NUMBER: PCT/US99/1355
PRIOR PELLOATION NUMBER: PCT/US99/1365
PRIOR PELLOATION NUMBER: PCT/US99/1365
PRIOR PELLOATION NUMBER: PCT/US99/1365
PRIOR PELLOATION NUMBER: PCT/US99/139
PRIOR PELLOATION NUMBER: PCT/US99/1309
PRIOR PELLOATION NUMBER: PCT/US99/1309
PRIOR PELLOATION NUMBER: PCT/US99/1309
PRIOR PELLOATI
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Patent No. US20020164646A1
GENERAL INFORMATION:
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Best Local Similarity 50.0%;
Matches 9; Conservative
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US-10-033-245-11
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Gaps

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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same File Reference: p293/011/6 CURRENT APPLICATION NUMBER: US/10/033,301 CURRENT FILING DATE: 2001-12-27
                                                                                                                                                                                                         Score 51; DB 12; Length 325;
Pred. No. 38;
1; Mismatches 8; Indels
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PRIOR PRICATION NUMBER: 60/095,325

PRIOR PILING DATE: 1998-08-04

PRIOR PILING DATE: 1998-12-16

PRIOR PELING DATE: 1998-12-16

PRIOR PELING DATE: 1998-12-16

PRIOR PELING DATE: 1998-12-16

PRIOR PELING DATE: 1998-12-22

PRIOR PELING DATE: 1998-12-22

PRIOR PELING DATE: 1999-01-12

PRIOR PELING DATE: 1999-02-10

PRIOR PELING DATE: 1999-02-10

PRIOR PELING DATE: 1999-02-12

PRIOR PELING DATE: 1999-10-29

PRIOR PELING DATE: 1999-10-39

PRIOR PELING DATE: 1999-10-39
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PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: PCT/US00/03565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 11, Application US/10033301
Patent No. US20020098506A1
GENERAL INFORMATION:
                                                                                                                                                                                                            Query Match
Best Local Similarity 50.0%;
Matches 9; Conservative
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Stewart, Timothy A.
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 11
LENGTH: 325
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Ferrara, Napoleone
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Wood, William I.
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Goddard, Audrey
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                                                                                                                          ORGANISM: Homo sapiens
US-10-033-246-11
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US-10-033-301-11
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APPLICANT:
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2930R1C12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/033,246
CURRENT FILING DATE: 2001-12-28
PRIOR PLICATION NUMBER: 60/095,325
PRIOR FLILING DATE: 1998-08-04
PRIOR FILING DATE: 1998-12-16
PRIOR FILING DATE: 1998-12-16
PRIOR PLICATION NUMBER: 60/113,145
PRIOR PLICATION NUMBER: 60/113,145
PRIOR PLICATION NUMBER: 60/113,15
PRIOR FILING DATE: 1998-12-16
PRIOR PLICATION NUMBER: 60/113,511
PRIOR FILING DATE: 1998-12-22
PRIOR PRIOR PRIOR DATE: 1999-01-12
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R FILING DATE: 2000-02-11

R APPLICATION NUMBER: PCT/USO0/04144

R FILING DATE: 2000-02-22

NR APPLICATION NUMBER: PCT/USO0/05841

R FILING DATE: 2000 -03-02

NR APPLICATION NUMBER: PCT/USO0/08439

NR FILING DATE: 2000-03-30

NR APPLICATION NUMBER: PCT/USO0/184941

R FILING DATE: 2000-05-30

R FILING DATE: 2000-05-30
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APPLICATION NUMBER: PCT/US99/12252
FILING DATE: 1999-06-02
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FILING DATE: 1999-12-01
APPLICATION NUMBER: PCT/US99/28551
FILING DATE: 1999-12-02
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PRIOR FILING DATE: 2000-06-02
PRIOR APPLICATION NUMBER: PCT/US00/32678
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R APPLICATION NUMBER: 60/162,506
R PILING DATE: 1999-10-29
R APPLICATION NUMBER: 60/170,262
R FILING DATE: 1999-12-09
R APPLICATION NUMBER: 60/187,202
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FILING DATE: 1999-01-12
APPLICATION NUMBER: 60/115,733
FILING DATE: 1999-01-12
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APPLICATION UNDBER: 60/119,537

RILING DATE: 1999-02-01

APPLICATION NUMBER: 60/119,965
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                                                                                                                                                                                 Sequence 11, Application US/10033246
Patent No. US2002098505A1
GENERAL INFORMATION:
APPLICANT: BOtstein, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stewart, Timothy A. Tumas, Daniel
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                                   270 CPICKNGPNCFAETAVIP 287
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Gao, Wei-Qiang
Goddard, Audrey
Gurney, Austin L.
Pan, James
| 25 CSICSNNPTCWAICKRIP 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roy, Margaret Ann
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                                                                                                                                RESULT 8
US-10-033-246-11
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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US-09-864-761-48887

Sequence 48887, Application US/09864761

Sequence 48887, Application US/09864761

Sequence 48887, Application US/09864761

Sequence 48887, Application US-09864761

Septem No. US200200487631

APPLICAWT: Penn, Sharron G.

APPLICAWT: Rank, David R.

APPLICAWT: Rank, David R.

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL FOR INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USFFUL STILE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXPRESSION ANALYSIS BY MICROARRAY

TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY

FILE REFERENCE Acond-Car x-1

CURRENT APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-08-03

PRIOR FILING DATE: 2000-10-04

PRIOR FILING DATE: 2000-10-130

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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Pred. No. 38;
1; Mismatches 8; Indels
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: 60/170,262
PRIOR PILING DATE: 1999-12-09
PRIOR PILING DATE: 2000-03-03
PRIOR FILING DATE: 2000-03-03
PRIOR PLICATION NUMBER: CT/US99/1252
PRIOR PLICATION NUMBER: PCT/US99/1252
PRIOR PPLICATION NUMBER: PCT/US99/28634
PRIOR PLILNG DATE: 1999-12-01
PRIOR PLILNG DATE: 1999-12-02
PRIOR PLILNG DATE: 1999-12-02
PRIOR PLILNG DATE: 1999-12-02
PRIOR PLILNG DATE: 2000-02-11
PRIOR PLILNG DATE: 2000-02-11
PRIOR PLILNG DATE: 2000-02-12
PRIOR PLILNG DATE: 2000-02-13
PRIOR PLILNG DATE: 2000-03-02
PRIOR PLILNG DATE: 2000-03-02
PRIOR PLILNG DATE: 2000-03-03
PRIOR PLILNG DATE: 2000-03-03
PRIOR PLILNG DATE: 2000-03-03
PRIOR PLILNG DATE: 2000-03-03
PRIOR PLILNG DATE: 2000-03-30
PRIOR PLILNG DATE: 2000-03-30
PRIOR PLILNG DATE: 2000-05-30
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50.0%;
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Best Local Similarity 50.0
Matches 9; Conservative
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US-09-864-761-48887
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LENGTH: 325
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Pred. No. 38;
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                        PRIOR FILING DATE: 2000-02-22
PRIOR PELICATION NUMBER: PCT/USOO/06414
PRIOR FILING DATE: 2000-03-22
PRIOR PELICATION NUMBER: PCT/USOO/05841
PRIOR PELICATION NUMBER: PCT/USOO/08439
PRIOR PLICATION NUMBER: PCT/USOO/08439
PRIOR PLICATION NUMBER: PCT/USOO/14941
PRIOR PLICATION NUMBER: PCT/USOO/15264
PRIOR PLICATION NUMBER: PCT/USOO/15264
PRIOR PLILING DATE: 2000-06-02
PRIOR PLILING DATE: 2000-06-05
PRIOR PLILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 38
SEQ ID NO 11
LENGTH: 325
TYPE: PRI
TYPE: PRI
TYPE: HOMO SAPIENS
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CURRENT FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/095,325
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PRIOR APPLICATION NUMBER: 60/112,851
PRIOR FILING DATE: 1998-12-16
PRIOR FILING DATE: 1998-12-16
PRIOR FILING DATE: 1998-12-16
PRIOR FILING DATE: 1998-12-2
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: 60/113,511
PRIOR APPLICATION NUMBER: 60/115,558
PRIOR APPLICATION NUMBER: 60/115,569
PRIOR FILING DATE: 1999-01-12
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APPLICATION NUMBER: 60/119,965
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/115,733
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.7%;
50.0%;
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Stewart, Timothy A.
Tumas, Daniel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gao, Wel-Qiang
Goddard, Audrey
Gurney, Austin L.
Pan, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Watanabe, Colin K.
         PRIOR FILING DATE: 2000-02-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1999-01-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 CPICKNGPNCFAETAVIP 287
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 50.0
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Desnoyers, Luc
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US-10-033-326-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-033-301-11
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Gaps

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APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL MO
TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISSPROT HIT: P14077, EVALUE 1.00e-09
EST_HUMAN HIT: AA668227.1, EVALUE 1.00e-34
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D IN HEART, SIGNAL = 1.2

D IN BONE MARNOW, SIGNAL = 1.5

D IN BONE ARROW, SIGNAL = 1.5

D IN LUNG, SIGNAL = 0.91

D IN LUNG, SIGNAL = 1.6

D IN ADULT LIVER, SIGNAL = 2.8

D IN BETAL LIVER, SIGNAL = 0.99

D IN FETAL LIVER, SIGNAL = 1.4

D IN HELA, SIGNAL = 1.7
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PRIOR FILING DATE: 2000-09-21
PRIOR PLILICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2001-06-30
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers: 1.1
SEQ ID NO 35081
LENGTH: 102
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CURRENT APPLICATION NUMBER: US/09/664,761
CURRENT FILING DATE: 2001-05-23
PRIOR PEDLICATION NUMBER: US 60/180,312
PRIOR PELLING DATE: 2000-02-04
PRIOR PELLING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/23,366
PRIOR PELLING DATE: 2000-10-04
PRIOR PELLING DATE: 2000-09-27
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR PELLING DATE: 2001-01-30
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PRIOR FILING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR PELLING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR PILLING DATE: 2001-01-30
PRIOR PLILNG DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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                                                    Sequence 35081, Application US/09864761
Patent No. US20020048763A1
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ORGANISM: Homo sapiens
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3
OTHER INFORMATION: EST_HUMAN HIT: BF220308.1, EVALUE 5.00e-16
OTHER INFORMATION: SWISSPROT HIT: P36627, EVALUE 4.30e-01
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PRIOR PLING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-21
PRIOR PLING DATE: 2000-09-30
PRIOR PLING DATE: 2000-06-30
PRIOR PLING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NOS: 49887
LENGTH: 35
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Pred. No. 4.3;
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Pred. No. 8.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Wong, James F.
APPLICANT: Wong, James F.
TITLE OF INVENTION: SCORPION TOXINS
FILE REFERENCE: BB1367 US NA
CURRENT FILING DATE: 2002-01-11
PRIOR APPLICATION NUMBER: 09/599,416
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR APPLICATION NUMBER: 60/140,227
PRIOR FILING DATE: 1999-06-22
NUMBER OF SEQ ID NOS: 28
SOFTWARE: MICTOSOFT Office 97
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                     R APPLICATION UNDBER: PCT/USO1/00668
R APPLICATION UNDBER: PCT/USO1/00668
R FILING DATE: 2001-01-30
R APPLICATION NUMBER: PCT/USO1/00661
R APPLICATION NUMBER: PCT/USO1/00670
R APPLICATION NUMBER: PCT/USO1/00670
R APPLICATION NUMBER: PCT/USO1/00670
APPLICATION NUMBER: PCT/US01/00665
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Patent No. US20020160454A1
GENERAL INFORMATION:
APPLICANT: Herrman, Rafael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28 CSNNPTCWAICKRIPNKKPGK 48
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26.1%;
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; ORGANISM: Hottentotta judaica
US-10-044-359-16
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Best Local Similarity 33.3%;
Matches 7; Conservative
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ORGANISM: Homo sapiens
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LENGTH: 58
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Length 102;

DB 10;

Score 50;

17.48;

Query Match

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APPLICANT: Gee, Melissa
APPLICANT: Tilotson, Bonnie
APPLICANT: Chang, Xiao-Jia
TITLEOF INVENTION: Systems for Sensitive Detection of G-Protein Coupled
TITLE OF INVENTION: Receptor and Orphan Receptor Function Using Reporter
TITLE OF INVENTION: Enzyme Mutant Complementation
TITLE OF INVENTION: Enzyme Mutant Complementation
FILE REFERENCE: 4085-235-27 CIP
CURRENT APPLICATION NUMBER: US/09/759,152
CURRENT APPLICATION NUMBER: US 09/654,499
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-07
PRIOR FILING DATE: 2000-09-07
NUMBER OF SEQ ID NOS: 9
SEQ ID NOS: 9
SEQ ID NO 2
LENGTH: 1010
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                           Gaps
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17.4%; Score 50; DB 10; Length 1024;
Best Local Similarity 38.7%; Pred. No. 1.7e+02;
Matches 12; Conservative 3; Mismatches 10; Indels
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                           Indels
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US-09-879-257A-30
Sequence 30, Application US/09879257A
Sequence 30, Application US/09879257A
Sequence 30, Application US/09879257A
Sequence 30, Application US/09879257A
GENERAL INFORMATION:
APPLICANT: YAMAMOTO, SACHIKO
APPLICANT: SHIRO, MINORU
APPLICANT: SHIRO, MINORU
SAPLICANT: KOBATAKE, SHIRO
FILE REPERENCE: 55986(70281)
CURRENT APPLICATION HUMBER: US/09/879, 257A
CURRENT FILING DATE: 2001-06-12
NUMBER OF SEC ID NOS: 56
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 30
LUMBER OF SEC ID NOS: 56
SOFTWARE: PATENTIN VER. 2.1
TYPE: PRT
TYPE: PRT
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  30.0%; Pred. No. 15; tive 4; Mismatches
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                                                                                                                                                                                                                                    Sequence 2, Application US/09759152
Patent No. US20020038433A1
GENERAL INFORMATION:
APPLICANT: Palmer, Michelle A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT ORGANISM: Unknown FEATURE: TEATURE: OTHER INFORMATION: PICAST ALC. US-09-759-152-2
Best Local Similarity 30.09
Matches 12; Conservative
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US-09-759-152-2
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381 KQNN-----FNAVRCSHYPNHPLWYTLCDR 405
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Search completed: November 22, 2002, 14:30:23 Job time : 12 secs

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COMPOTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                          :Patent No. 5194595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;SEQ ID NO:19:
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US-08-467-963C-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYNCYTIAL VIRUS
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5, Appli
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                                                                                                       November 22, 2002, 14:25:06; Search time 15 Seconds (without alignments) 96.115 Million cell updates/sec
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Compugen Ltd
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US-08-793-792-3
US-09-248-588-53
US-08-793-792-13
PCT-US91-08177-13
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US-08-846-344 D-8
US-08-344 C-969A-8
US-08-467-969A-8
US-08-00-554A-8
US-08-793-792-12
US-08-793-792-4
US-08-793-792-4
US-08-793-792-4
US-08-750-624-9
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S-08-793-792-7
S-08-750-624-10
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                                                                                                                                                                                                                                                                                         262574 segs, 29422922 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUMMARIES
      GenCore version Copyright (c) 1993 - 2002
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Maximum Match 100%
Listing first 45 summaries
                                                                          protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Match Length DB
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288
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Perfect score:
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                                                                          OM protein
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Maximum DB
                                                                                                                                                                                                           Sequence:
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1, Appl
1, Appl
19, Appl
19, Appl
11, Appl
11, Appl
11, Appl
11, Appl
11, Appl
8, Appl
8, Appl
8, Appl
8, Appl
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Patent No. 5968776
GENERAL INFORMATION:
APPLICANT: INFORMATION:
APPLICANT: DU, Run-Pan
APPLICANT: EMASYSHYN, MATY E
APPLICANT: EMASYSHYN, MATY E
ATTLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
AUTHERN OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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TITLE OF INVENTION: CHIMERIC GLYCOPROTEINS CONTAINING; IMMUNGENIC SEGMENT OF THE GLYCOPROTEINS OF HUMAN RESPIRATORY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 288; DB 6; Best Local Similarity 100.0%; Pred. No. 1.7e-26; Matches 49; Conservative 0; Mismatches 0;
US-08-721-979A-20
US-08-836-501-20
US-08-84-299-20
US-08-793-792-9
US-08-793-792-9
US-08-793-792-9
US-08-721-979A-19
US-08-836-501-19
US-09-654-289-11
US-09-654-289-11
US-09-654-289-11
US-09-654-289-11
US-08-656-055-8
US-08-656-055-8
US-08-656-055-8
US-08-951-055-8
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STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 19
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/543,780
FILING DATE: 31-OCT-1988
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 137,387
FILING DATE: 23-DEC-1987
      NUMBER OF SEQUENCES: CORRESPONDENCE ADDRESS
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Gaps
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APPLICANT: KIEIN, Michel H
APPLICANT: EMASYSHYN, Mary E
APPLICANT: EWASYSHYN, Mary E
TITLE OF INVENTION: CHIMBERIC PROTEIN WHICH CONFERS PROTECTION
TITLE OF INVENTION: AGAINST PARAINFLUENZA VIRUS AND RESPIRATORY
TITLE OF INVENTION: SYNCYTIAL VIRUS
                                                                                                                                                                                                                                                                                                                                   ó
                                                                                                                                                                                                                                                                                      Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                    149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWALCKRIPNKKPGKK 197
                                                                                                                                                                                                                                                                                                                                                                              1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUFTWARE: Patentin Release #1.0, Version #1.30 CURENT APPLICATION DATA:
PILING DATE: 07-MAY-1997
CLASSIFICATION: 4.24
                                                                                                                                                                                                                                                                                   Score 285; DB 2;
Pred. No. 1.7e-26;
1; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 285; DB 3;
Pred. No. 1.7e-26;
                        1038-687 MIS: jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: Sim & McBurney
6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,639
FILING DATE: 14-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 6th Floor, 330 University
CITY: TOCORCO
STATE: Ontario
COUNTRY: Canada
ZIP: M5G IR7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PARENTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 8, Application US/08852344D Patent No. 6017539
REGISTRATION NUMBER: 24,973
REFRENCE/DOCKET NUMBER: 1038
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 annino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: STEWART, Michael I
REGIESTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 101
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        99.0%;
98.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99.0%;
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Best Local Similarity 98.08
Matches 48; Conservative
                                                                                                                                                                                  single
linear
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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; TOPOLOGY: lin
US-08-838-189D-8
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US-08-852-344D-B
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US-08-852-344D-8
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APPLICANT: EWASYSHYN, Mary E
TITLE OF INVENTION: MULTIMERIC HYBRID GENE ENCODING A
TITLE OF INVENTION: CHIMBRIC PROPEIN WHICH CONFERS PROTECTION AGAINST
TITLE OF INVENTION: PARAINFLUENZA VIRUS AND RESPIRATORY SYNCYTIAL VIRUS
MYNBER OF SEQUENCES: 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKK 197
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    Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                     1038-474 MIS:jb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 1.76
1; Mismatches
                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/838,189
FILING DATE: 16-APP-1997
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
RECOR APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9200117.1
FILING DATE: 06-JAN-1992
ATTORNEY/AGENT INFORMATION:
                        URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,963C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
| APPLICATION NUMBER: US/08/838,189D|
| FILLION DATE: 16-APR-1997|
| CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 8, Application US/08838189D Patent No. 5998169
GENERAL INFORMATION:
APPLICANT: KLEIN, Michel H
APPLICANT: DU, Run-Pan
APPLICANT: EWASYSHYN, MAIY E
                                                                                                                                                                                                                                                                                                        NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
I REFERENCE/DOCKET NUMBER: 103
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 298 amino acids
TYPE: amino acid
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STEWART, Michael I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 48; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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ZIP: M5G 1R7
                                                                                          CLASSIFICATION:
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            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:

APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: CHIMERIC PROTEIN WHICH CONFERS
TITLE OF INVENTION: PROTECTION AGAINST PARAINFLUENZA VIRUS
TITLE OF INVENTION: AND RESPIRATORY SYNCYTIAL VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 298;
                                                                        149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
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        0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: THEN PC COMPATIBLE
COMPUTER: THEN PC COMPATIBLE
COMPUTER: THEN PC COMPATIBLE
COMPUTER: PATENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/08/344,639E
FILING DATE: 14 NOV-1994
CLASSIFICATION DATA:
APPLICATION NUMBER: US 08/001,554
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEAMT, MINER: 424
ATTORNEY/AGENT INFORMATION:
NAME: STEAMT, MINER: 1038-391 MIS
TELECOMMUNICATION NUMBER: 1038-391 MIS
TELECOMMUNICATION INFORMATION:
THE FORMATION INFORMATION:
THE POLICE THE POLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 99.0%; Score 285; DB 3; Ls Best Local Similarity 98.0%; Pred. No. 1.7e-26; Matches 48; Conservative 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Sim & MCBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
STATE: Ontario
STOWNEY: Canada
    1; Mismatches
                                                                                                                                                                                                                                                                                                                                                   Sequence 8, Application US/08344639E Patent No. 6033668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08467969A Patent No. 6168786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-344-639E-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELER: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 298 amino acids
48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-08-467-969A-8
                                                                                                                                                                                                                                                                                                               US-08-344-639E-8
    Matches
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 KORONKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                               ZIP: MSG IR7

ZIP: MSG IR7

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,969A
                                                                                                                                     ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 8, Application US/08467961A
Patent No. 6171783
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCBurney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6TH Floor
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Ewasyshyn, Mary E
TITLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIPTCATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION A35
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION UNMBER: GB 9200117.1
FILING DATE: 06-TAN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: STEWATE, Michael I
REGISTRATION NUMBER: 24,973
                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US/08/467,969A
06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 1031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : 298 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
                                                                                                                                                                                                         Ontario
: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 06 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Toronto
STATE: Ontario
COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                               CITY: TOR
STATE: On
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-467-961A-8
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TITLE OF INVENTION: Antigenic peptides derived from the TITLE OF INVENTION: G-protein of RSV for type- and subtype-specific diagnosis TITLE OF INVENTION: of respiratory syncytial virus (RSV) infection. NUMBER OF SEQUENCES: 13 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                              Length 298,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 37;
                                                                                                                                                                                                                                                                                                                                                                                      1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PERITIN Release #1.0, Version #1.30 (EPO)
CURREM APPLICATION DATA:
APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                            Score 285; DB 4; La
Pred. No. 1.7e-26;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 217; DB 3;
Pred. No. 2.4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9 SKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
TITLE OF INVENTION: Antigenic per TITLE OF INVENTION: G-protein of TITLE OF INVENTION: of respirate NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
COMPUTER: ISM PC COMPATIBLE
COMPUTER: ISM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
                       TELEPHONE: (416) 595-1153
TELEFA: (416) 595-1163
TELEFA: (6416) 595-1163
TELEA: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
STRANDEDNESS: single
      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                            Query Match 99.0%;
Best Local Similarity 98.0%;
Matches 48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 75.3%;
Best Local Similarity 97.3%;
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CIASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                        TOPOLOGY: 1 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 9
US-08-793-792-12
                                                                                                                                                                                                                                                      US-08-001-554A-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-793-792-12
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 149 KQRQNKPPNKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
| COMPUTER: IBM PC compatible
| OPERATING SYSTEM: PC-DOS/MS-DOS
| SOFTWARE: PATENTIN Release #1.0, Version #1.25
| CURRENT APPLICATION DATA: US/08/001,554A
| FILING DATE: 06-JAN-1993
                                                                                      | SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 8, Application US/08001554A
Patent No. 6225091
GENERAL INFORMATION:
APPLICANT: Klein, Michel H
APPLICANT: Du, Run-Pan
APPLICANT: Du, Run-Pan
APPLICANT: Ewsyshyn, Mary E
TTLLE OF INVENTION: Chimeric Immunogens
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & McBurney
STREET: 330 University Avenue, 6th Floor
CITY: Toronto
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-476 MIS:bh
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                             APPLICATION NUMBER: US/08/467,961A FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                  FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/001,554
FILING DATE: 06-JAN-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,913
REFERENCE/DOCKET NUMBER: 1038-286
                                                                                                                                                                                                                                                      | CLASTECATION:
| CLASTECATION:
| PRIOR APPLICATION DATA:
| APPLICATION NUMBER: GB 9200117.1 |
| FILING DATE: 06-JAN-1992 |
| FILING DATE: 435-JAN-1992 |
                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
TELEX: 065-24567 SIMBAS
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
COMPUTER READABLE FORM:
| MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ontario
: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: M5G 1R7
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COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48;
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Sequence 9, Application US/08750624

Sequence 9. Application US/08750624

GENERAL INFORMATION:
APPLICANT: Kandil, Ali
APPLICANT: Chong, Pele
APPLICANT: Klein, Michel H
ATITLE OF INVENTION: ADJUVANT COMPOSITIONS COMPRISING A
TITLE OF INVENTION: ADJUVANT COMPOSITIONS COMPRISING A
TITLE OF INVENTION: MINERAL SALT AND ANOTHER IMMUNOSTIMULATING COMPOUND
NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.7%; Score 146; DB 4; Length 26; 100.0%; Pred. No. 4.4e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,624
                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 151; DB 3;
Pred. No. 1.6e-11;
4; Mismatches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 KPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKK 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KPKDDYHFEVFNFVPCSICGNNQLCKSICKTIPSNK 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Sim & McBurney
STREET: 6th Floor, 330 University Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/750,624
FILING DATE: 26-FEB-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I
REGISTATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-660
FELECOMMNICATION INFORMATION:
                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER REDAM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                          52.4%;
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TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                 CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 69.49
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 26 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                           TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                           ) MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
US-08-793-792-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Sim & MCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Canada
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                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-750-624-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-750-624-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antigenic peptides derived from the G-protein of RSV for type- and subtype-specific diagnosis of respiratory syncytial virus (RSV) infection.
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                       SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: Antigenic peptides derived from the TITLE OF INVENTION: G-protein of RSV for type- and substitute OF INVENTION: of respiratory syncytial virus (RS) NUMBER OF SEQUENCES: 13
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   Query Match 67.0%; Score 193; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.4e-16;
Matches 32; Conservative 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 60.4%; Score 174; DB 3; Best Local Similarity 100.0%; Pred. No. 2.3e-14 Matches 28; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10 KPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11 PNNDFHFEVFNFVPCSICSNNPTCWAIC 38
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Patent No. 6077511
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: G-protein of RG;
TITLE OF INVENTION: G-protein of RG;
TITLE OF INVENTION: of respiratory
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-793-792-4; Sequence 4, Application US/08793792; Patent No. 6077511; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                            CLASSIFICATION: 514
INPORMATION FOR ESQ ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 28 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide HYPOTHETICAL: NO
    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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                                                                                              FILING DATE:
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US-08-793-792-11
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Gaps ö

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Search completed: November 22, 2002, 14:27:20 Job time : 16 secs
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MOLECULE TYPE: pept
HYPOTHETICAL: NO
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STRANDEDNESS: si
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                                                                                                                                                                                                                                          APPLICANT: Binz, Hans
APPLICANT: Nguyen Ngoc, Thien
APPLICANT: Stain, Stefan
APPLICANT: Stain, Stefan
APPLICANT: Uhlen, Mathias
APPLICANT: Nygren, Per Ake
TITLE OF INVENTION: Method for obtaining a peptide derived
TITLE OF INVENTION: from the respiratory syncytial virus, polypeptide and
TITLE OF INVENTION: medicinal product.
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89.7%; Pred. No. 6.6e-11;
.ive 0; Mismatches 3; Indels
  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Rockey, Milnamow & Katz
STREET: 180 N. Stetson Avenue, 2 Prudential Plaza,
STREET: Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/08/836,504A
FILING DATE: 07-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Katz, Martin L.
REGISTRATION NUMBER: 25,011
FEEDENOMAUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: 312-616-5400
  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21 NFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08793792
Patent No. 6077511
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Antigenic pept
TITLE OF INVENTION: Of respirator)
TITLE OF INVENTION: Of respiratory
                                  1 KORONKPPSKPNNDFHFEVFNFVPC 25
                                                           2 KQRQNKPPSKPNNDFHFEVFNFVPC 26
                                                                                                                                                                                  Sequence 6, Application US/08836504A Patent No. 6130091 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 30 amino acids TYPE: amino acid
25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CORRESPONDENCE ADDRESS:
ADDRESSEE: ROCKEY, M
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TOPOLOGY: line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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                                                                                                                                                               US-08:836-504A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
US-08-793-792-7
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  Matches
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                                                                                                                                            RESULT 14
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Gaps
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NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/08/793,792
                                                                                                                                                                                                                                                                                                                                                              Score 138; DB 3; Le
Pred. No. 4.8e-10;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KPKDDYHFEVFNFVPCSICGNNOLCKSICKTI 32
                                                                                                                                                                                                                                                                                                                                                                                                                                     10 KPNNDFHFEVFNFVPCSICSNNPTCWAICKRI 41
                                                                                                                                                                                                                                                                                                                                                                47.9%;
71.9%;
                                                                                                                                                                                                                                                                                                                                                              Query Match 47.9%
Best Local Similarity 71.99
Matches 23; Conservative
                                                                                                                                             FILING DATE:
CLASSIFICATION: 514
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
                                                                                                                                                                                                                                                                              . peptide
NO
                                                                                                                                                                                                                                                           single
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(without alignments)
186.551 Million cell updates/sec
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1 KQRQNKPPSKPNNDFHFEVF......NNPTCWALCKRIPNKKPGKK
                                                                                                                November 22, 2002, 14:16:41; Search time 35 Seconds
                                                                                                                                                                                                                                                                                                                                                                                        908470
GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                              908470 segs, 133250620 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                              - protein search, using sw model
                                                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 200000000
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Perfect score:
Sequence:
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                                                                              OM protein
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/SIDS2/gcgdata/geneseq/geneseqp·embl/AA2000.DAT:*/SIDS2/gcgdata/geneseq/geneseqp·embl/AA2001.DAT:*/SIDS2/gcgdata/geneseq/geneseqp·embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:* /SIDS/gcgdata/geneseq/geneseqp embl/AA1982.DAT:*/SIDS/gcgdata/geneseq/geneseqp embl/AA1983.DAT:*/SIDS/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*/SIDS/gcgdata/geneseq/geneseqp-embl/AA1984.DAT:*/SIDS/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS/gcgdata/geneseq/geneseqp-embl/AA1986.DAT:*/SIDS/gcgdata/geneseq/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/geneseqg/geneseqp-embl/AA1987.DAT:*/SIDS/gcgdata/g /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1996. /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1991 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1992 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1993 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1994/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1995 /SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1998 /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999 /SIDS2/gcgdata/geneseq/genesegp-embl/AA1980. /SIDS2/gcgdata/geneseg/genesegp-embl/AA1981. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1997 A_Geneseq_101002: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		Description		Human KSV A Subtyp	Human RSV G protei	Sequence of human	HSRV qlycoprotein	HRSV alycoprotein	Respiratory syncyt	Chimeric human res			
		QI		AAM3921/	AAW39244	AAW39248	AAW39250	AAW39251	AAP70845	AAR25302	AAW47605	AAU74676	AAP90441
		DB		1	19	19	19	19	8	13	19	23	10
		Match Length DB		4	49	49	49	49	298	298	298	298	681
æ	Query	Match		100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
		Score	0000	007	288	288	288	288	288	288	288	288	288
	Result	No.		4	7	ო	4	2	9	7	8	0	10

WPI; 1998-042117/04

Gorman JJ;

RSV A RSV A RSV A RSV A	Hamman Ray & Subcyt Respiratory Syncyt RSV G protein anti Anino acid sequenc Respiratory Syncyt RSV G protein anti	0 2 2 2 2 2 3	peptide acid sec acid sec acid sec acid sec acid sec acid sec acid sec	Streptococcal prot Amino acid sequenc Amino acid sequenc Amino acid sequenc Human RSV A subtyp Respiratory Syncyt RSV G protein anti Amino acid sequenc Peptide which indu Respiratory Syncyt RSV G protein anti
AAW39218 AAW39219 AAW39221 AAW39222 AAW39223	AAR97073 AAR97073 AAY44100 AAB84145 AAR97072 AAY44099	AAR84144 AAR88253 AAR95610 AAR95616 AAR97050	AAB18805 AAG67741 AAB84123 AAB68016 AAB67775 AAW96314 AAR39286 AAW96313	AAR95660 AAB68028 AAB68028 AAM39220 AAR97074 AAY44101 AAB84146 AAB91015 AAR97075
61116	20 20 17 20 20	110 117 117 117	222 222 223 24 203 203 203 203 203 203 203 203 203 203	17 22 22 113 22 20 20 20
4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	9 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	101	101 101 101 101 232 298 298	349 349 452 49 57 57 57 101 55 55
				999.0 999.0 997.2 93.8 93.4
7 5 8 2 2 2 8 2	7 5 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	5 8 2 2 2 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3	2822 2822 2822 2822 2822 2822 2822 282	00000000000000000000000000000000000000
1122	16 18 20 21	22 2 3 3 2 4 3 2 5 4 3 3 5 4 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3 3 3 3 3 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	3 3 3 3 4 4 4 4 4 4 4 4 5 5 5 5 5 5 5 5

ALIGNMENTS

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G protein; treatment; prevention; diagnosis; infection; immunity; antibody; Pneumovirus; identification; vaccine; cell receptor.
                                                               Human RSV A subtype G protein fragment (aa. 149-157) strain A2.
                                                                                                                                Location/Qualifiers
25..38
28..34
                                                                                                                                                                                                                                                    (BIOM-) BIOMOLECULAR RES INST LTD.
                                                                                                               Human respiratory syncytial virus.
         AAW39217 standard; peptide; 49 AA.
                                                                                                                                                                                                            97WO-AU00351.
                                                                                                                                                                                                                                96AU-0000265.
                                              27-AUG-1998 (first entry)
                                                                                                                                           Disulfide-bond
Disulfide-bond
                                                                                                                                                                       WO9746581-A1.
                                                                                                                                                                                                             04-JUN-1997;
                                                                                                                                                                                                                                05-JUN-1996;
                                                                                                                                                                                          11-DEC-1997.
                            AAW39217;
AAW39217
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                                                               AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
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                                                                                                                                                                                                                                Gaps
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Peptide(s) derived from specific region of respiratory syncytial virus G protein – used to treat, prevent, diagnose and immunise
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                                                                                                                                                                                                          Length 49;
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                                                                                                                                                                                                                                                                                                                                                                                                         Human RSV G protein fragment (aa. 149-157) derivative #1.
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                                                                                                                                                                                                        Score 288; DB 19;
Pred. No. 2.2e-28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human respiratory syncytial virus.
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                                                                                                                                                                                                        100.0%;
             virus G protein – used to trea
against Pneumovirus infection
                                            Claim 5; Fig 2; 75pp; English.
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AAW39244-W39252 are derivatives of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used to identify compounds able to inhibit binding of RSV to host cells and for characterisation of call receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human RSV G protein fragment (aa. 149-157) derivative #5.
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                                                                                                                                                                                                                                                                                ; DB 19;
2.2e-28;
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                                                                                                                                                                                                                                                                                Score 288;
Pred. No. 2.
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                                                                                                                                                                                                                                                                             100.0%; Sc
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ive 0;
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Best Local Similarity
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(first entry)

diagnosis; infection; immunity;

'note= "N-terminal biot group"

Location/Qualifiers

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G protein; treatment; prevention; diagnosis; infection; immuniantibody; Pneumovirus; identification; vaccine; cell receptor.
                                                                                                                                                                                                                                               Human RSV G protein fragment (aa. 149-157) derivative #8.
                                                                                                                                                                                                                                                                                                                                                                                                           Human respiratory syncytial virus.
                                                                AAW39251 standard; peptide; 49
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Disulfide-bond
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                                                                    Gaps
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                                                                                                                           1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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                                                                Indels
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llarity 100.0%; Pred. No. 2.2e-28;
Conservative 0; Mismatches 0;
Score 288; DB 19;
Pred. No. 2.2e-28;
Mismatches 0;
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28..34
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   Query Match
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AAW39244-W39252 are derivatives of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used conformed able to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
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illarity 100.0%; Pred. No. 2.2e-28;
Conservative 0; Mismatches 0;
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Best Local Similarity
Matches 49; Conserv
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WO9746581-A1
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Gaps

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The sequences of mRNA encoding HRSV structural proteins are given in AAQ2562-28. The proteins are F, G, 22K, 9.5K and major capsid protein N. The sequences and encoded proteins are useful for preparing vaccines against HRSV. The vaccines can be used to confer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Production of human respiratory syncytial virus glyco-protein F or (
- by culturing eukaryotic host cells transfected with corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for the production of human respiratory syncytial virus (HRSV) glycoprotein F (gpF) or glycoprotein G (gpG). The method comprises culturing eukaryotic host cells transfected with an isolated DNA sequence encoding HRSV gpF or gpG. The gp can be used to prepare vaccines against HRSV.
                                                                                                                                                                                         immunity against respiratory tract infections on human subjects
                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                      Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence was used in the development of a novel
                              Vaccines for human respiratory virus – include structural ge coding for native structural viral proteins and immunogenic
                                                                                                                                                                                                                                                                                                                                        149 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKFGKK 197
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRSV; glycoprotein F; gpF; glycoprotein G; gpG; vaccine.
                                                                                                                                                                                                                                                                                                                         1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
                                                                                                                                                                                                                                                      Score 288; DB 13;
Pred. No. 1.4e-27;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Columns 27-28; 17pp; English.
                                                                                             Disclosure; Page 18; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human respiratory syncytial virus.
                                                                                                                                                                                                                                                   100.0%; Sci
100.0%; Pr
vative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW47605 standard; Protein; 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (PHAA ) PHARMACIA & UPJOHN CO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88US-0218737.
86US-0818740.
86WO-US02756.
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97US-0854783
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                                                                                                                                                                                                                                                                                         49; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wertz GW;
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                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 49; Conserv
                                                                                                                                                                                                                            298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HRSV glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA;
N-PSDB; AAQ29623.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US5716823-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-FEB-1998
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                                                                 fragments
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW47605;
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                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 8
AAW47605
Dp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; human respiratory syncytial virus; HRSV; F; G; 22K; 9.5K; major capsid protein; N.
                                                                                                                                                                                                                                                                                                                                                                                                                                A novel plasmid which comprises a DNA sequence encoding this protein, and the protein itself, are claimed, for use as HRSV yaccines. The vaccine can be administered to pregnant women or women of child bearing age to stimulate maternal antibodies. Infants can also be vaccinated at 2-3 months of age.
                                                                                                                                                                                                                                                                                                                                      Accines for human respiratory virus - comprising proteins or ragment encoded by a DNA sequence coding for human respiratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 298;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 288; DB 8;
ilarity 100.0%; Pred. No. 1.4e-27;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human respiratory syncytial virus strain A2
                                                             Juman respiratory syncytial virus (HRSV)
                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Chart 13; 57pp; English.
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                                                                                                                                                         86WO-US02756
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                                                                                                                                                                                                                     (UYNC-) UNIV OF N CAROLINA.
(WERT/) WERTZ G W.
(WERT/) WERTZ G W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSRV glycoprotein G (gpG).
                                                                                                                                                                                                                                                                                                                                                                        syncytial virus proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wertz GW;
                                                                                                                                                                                                                                                                                        WPI; 1987-206300/29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 298 AA;
                                                                                                                                                                                                                                                                                                        N-PSDB; AAN70784.
                                                                                                                                                           3-DEC-1986;
                                                                                                                                                                                         4-JAN-1986;
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                                                                                          VO8704185-A
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                                                                                                                           6-JUL-1987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                49;
protein.
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                              'accine
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Matches
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suitable for expression by the recombinant virus of the invention.

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comprising neutron teraction teractions are recombinant virus comprising an antiquence fragment. The virus may be administered in combination with an antifytral chamchterapeutic compound. Two or more viruses expressing different PMV proteins nay be co-administered. Compositions comprising the virus are useful for eliciting a humoral and/or cellular immune response to a PMV in a mammal, particularly a human. Further a recombinant Sendai virus comprising an exogenous nucleic acid encoding a second PMV protein is also administered and priming and/or boosting humoral or cellular immune response comprises administering one or more of a recombinant or isolated PMV protein or its antigenic fragment, a DNA vaccine encoding the same, and a non-Sendai viral vector encoding a PMV protein. The recombinant virus is useful as an effective encoding a PMV protein. The recombinant virus is useful as an effective encoding a part and also to express of paediatric respiratory disease) and also to express of edical impact on into stem cells. Wild-type globin gene transfer (i.e. gene therapy) into stem cells. Wild-type globin gene transfer (i.e. gene therapy) into stem cells effects a cure for sickle cell disease or betathal assammia. The recombinant virus may also prove effective in conferring immunity to human immunodeficiency virus (HIV) infection. The sendai virus replicates at level that is high enough to human recipient. The present sequence represents a respiratory syncytial virus (RSV) G protein (heavily glycosylated protein), a PMV protein
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                                                                                                                                                                                                                                                                                                                                                                                                  protein; heavily glycosylated protein; antianaemic; antiviral;
                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant Sendai virus useful in vaccines to protect infection by paramyxoviruses, comprises exogenous nucleic acid encoding paramyxovirus protein or its antigenic fragment -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a recombinant Sendai virus comprising an
                                                                                                                                                                                                                                                                                                                                                                                                               Vaccine; gene therapy; paramyxovirus; sendel virus; PWV; antiviral chemotherapeutic compound; humoral response; cellular immune response, hPIV; paediatric respiratory disease; globin gene transfer; sickle cell disease; beta-thalassaemia; human immunodeficiency virus infection; HIV.
                                             ö
Length 298;
                                                                                                          1 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                             Indels
    DB 19;
                        1.4e-27
                                           0; Mismatches
  100.0%; Score 288; 100.0%; Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                             Respiratory syncytial virus G protein.
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                                                                                                                                                                                                                                AAU74676 standard; Protein; 298 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human respiratory syncytial virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2000; 2000US-208701P.
                                                                                                                                                                                                                                                                                                                   (first entry)
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Portner A, Takimoto T;
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N-PSDB; AAS21045.
                        Similarity
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                                                                                                                                                                                                                                                                                                                 09-APR-2002
                                           49;
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  Query Match
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Matches
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                                                                   Gaps
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                                                                                                                                                                                                                                                  Chimeric human respiratory synctial virus glycoproteins F and G.
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                                          Length 298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chimeric human respiratory syncytial virus polypeptides(s) - contg. immunogenic fragments from HRSV glycoproteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       543 KORONKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 591
                                                                                                       149 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 197
                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
                                                                   Indels
                                                                                                                                                                                                                                                                     Chimeric polypeptide; human respiratory syncytial virus; protein F; protein G; vaccine.
                                                                                           1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK
                                          Score 288; DB 23;
Pred. No. 1.4e-27;
                                 100.0%; Scc. 100.0%; Pred. No. 1... 0; Mismatches
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100.0%; Pred. No. 3.
ive 0; Mismatches
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                                                                                                                                                                                                                                                                                                             Human respiratory syncytial virus.
                                                                                                                                                                            681
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                                                                                                                                                                           AAP90441 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                   88WO-US03784.
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                                                                                                                                                                                                                            (first entry)
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                                                                    Conservative
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Best Local Similarity
Matches 49; Conserv
                                                       Best Local Similarity
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                     298 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                 (UPJO ) UPJOHN CO.
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                                                                                                                                                                                                                          01-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                   31-OCT-1988;
                                                                                                                                                                                                                                                                                                                                                                                                           23-DEC-1987;
                                                                                                                                                                                                                                                                                                                                     WO8905823-A.
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                                                                    49;
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                      Seguence
                                             Query Match
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                                                                                                                                                      RESULT 10
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SXS
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W09746581-A1

04-JUN-1997; 05-JUN-1996;

Gorman JJ;

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1-DEC-1997

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AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human RSV A subtype G protein fragment (aa. 149-157) strain A6256.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; treatment; prevention; diagnosis; infection; immunity;
                                                                                                                                                                                                                                           Peptide(s) derived from specific region of respiratory syncytial virus G protein - used to treat, prevent, diagnose and immunise
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptide(s) derived from specific region of respiratory syncytial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody; Pneumovirus; identification; vaccine; cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KQRQNKPPSKPNNDFHFEVFNFVPCSICSNNPTCWAICKRIPNKKPGKK 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 285; DB 19;
Pred. No. 5.3e-28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
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                                                                                                                        LTD.
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                                                                                                                      (BIOM-) BIOMOLECULAR RES INST
                                                                                                                                                                                                                                                                                                                        Claim 5; Fig 2; 75pp; English.
                                                                                                                                                                                                                                                               virus G protein – used to trea
against Pneumovirus infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99.0%;
                                       97WO-AU00351
                                                                               96AU-0000265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAW39221 standard; peptide;
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                                                                                                                                                                                                 WPI; 1998-042117/04.
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Best Local Similarity
Matches 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49 AA;
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Disulfide-bond
                                       04-JUN-1997;
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Human RSV A subtype G protein fragment (aa 149–157) strain long A.
                                       G protein; treatment; prevention; diagnosis; infection; immunity;
antibody; Pneumovirus; identification; vaccine; cell receptor.
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Pred. No. 5.3e-28;
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                                                                                                 Juman respiratory syncytial virus.
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may allow a reduction in dose, and thus side effects, of the vaccine
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                                                              AAW39217-W39234 are fragments of the human respiratory syncytial virus (RSV) G protein corresponding to amino acids 149 to 197. These fragments can be used to treat, prevent or diagnose Pneumovirus, specifically RSV, infection and to immunise against such infections. Antibodies raised from these fragments may also be used diagnostically. The fragments may also be used diagnostically. The fragments may also be used to inhibit binding of RSV to host cells and for characterisation of cell receptors for Pneumoviruses. When the fragments are used in combination with existing vaccines, they may allow a reduction in dose, and thus side effects, of the vaccine.
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 virus G protein - used to treat, prevent, diagnose and immunise against Pneumovirus infection
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Pred. No. 5.3e-28;
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                                     Claim 5; Fig 2; 75pp; English.
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Pred. No. 5.3e-28;
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